

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 27, 2003, 01:09:38 / Search time 472 Seconds
(without alignments)
4111.382 Million cell updates/sec

Title: US-09-687-230a-2
Perfect score: 3073
Sequence: 1 MGKKKKKKSKDKHLYERYVE.....PGNNICLLGPSSKCIILINK 589

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2190069 segs, 1647345023 residues
Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cg2_1/USPTO.spool/p/US09667230/runat_25112003_123734_17741/app_query.fasta_1.775
-DB=Published Applications NA -QFMT=fastap -SUFFIX=nov25.tmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bases -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=human40.cdt -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

- 1: /cg2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cg2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cg2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cg2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cg2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cg2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 10: /cg2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 11: /cg2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 12: /cg2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cg2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cg2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cg2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cg2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cg2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3002.5	97.7	7053	10	US-09-764-864-792 Sequence 792, App

2	1263	41.1	1351	10	US-09-764-864-379 Sequence 379, App
3	921.5	30.0	2830	13	US-10-098-841-196 Sequence 196, App
4	872.5	28.4	517	10	US-09-867-701-2944 Sequence 2944, App
5	780	25.4	480	11	US-09-918-995-37236 Sequence 37236, App
6	502.5	16.4	421	10	US-09-960-352-7102 Sequence 7102, App
7	477	15.5	513	10	US-09-960-253-96 Sequence 96, App
8	359	11.7	7053	10	US-09-764-864-792 Sequence 792, App
9	274	8.9	1861	12	US-10-096-531-53 Sequence 53, App
10	258.5	8.4	4549	14	US-10-037-270-266 Sequence 266, App
11	258.5	8.4	4942	14	US-10-037-270-267 Sequence 267, App
12	227	7.4	8147	13	US-10-109-886-9 Sequence 9, App
13	219.5	7.1	1636	9	US-09-925-301-104 Sequence 104, App
14	215.5	7.0	577	9	US-09-864-761-11927 Sequence 11927, App
15	215.5	7.0	32222	14	US-09-764-887-619 Sequence 619, App
16	215.5	7.0	32222	14	US-10-073-961-619 Sequence 619, App
17	213.5	6.9	2232	9	US-09-864-761-28507 Sequence 28507, App
18	210	6.8	5959	10	US-09-954-456-1996 Sequence 1996, App
19	205	6.7	5257	12	US-10-007-926A-237 Sequence 237, App
20	205	6.7	7336	13	US-10-109-886-7 Sequence 7, App
21	201	6.5	2213	12	US-10-199-672-549 Sequence 549, App
22	201	6.5	2213	12	US-10-187-748-549 Sequence 549, App
23	201	6.5	2213	12	US-10-194-457-549 Sequence 549, App
24	201	6.5	2213	12	US-10-184-642-549 Sequence 549, App
25	201	6.5	2213	12	US-10-196-747-549 Sequence 549, App
26	201	6.5	2213	12	US-10-173-689-549 Sequence 549, App
27	201	6.5	2213	12	US-10-173-689-549 Sequence 549, App
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31	201	6.5	2213	12	US-10-173-698-549 Sequence 549, App
32	201	6.5	2213	12	US-10-173-699-549 Sequence 549, App
33	201	6.5	2213	12	US-10-173-707-549 Sequence 549, App
34	201	6.5	2213	12	US-10-174-569-549 Sequence 549, App
35	201	6.5	2213	12	US-10-174-583-549 Sequence 549, App
36	201	6.5	2213	12	US-10-174-589-549 Sequence 549, App
37	201	6.5	2213	12	US-10-174-591-549 Sequence 549, App
38	201	6.5	2213	12	US-10-174-591-549 Sequence 549, App
39	201	6.5	2213	12	US-10-175-736-549 Sequence 549, App
40	201	6.5	2213	12	US-10-175-742-549 Sequence 549, App
41	201	6.5	2213	12	US-10-175-744-549 Sequence 549, App
42	201	6.5	2213	12	US-10-175-748-549 Sequence 549, App
43	201	6.5	2213	12	US-10-175-748-549 Sequence 549, App
44	201	6.5	2213	12	US-10-175-751-549 Sequence 549, App
45	201	6.5	2213	12	US-10-175-754-549 Sequence 549, App

ALIGNMENTS

RESULT 1
US-09-764-864-792
Sequence 792, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764, 864
PRIORITY FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 792
LENGTH: 7053
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (154)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-792
Alignment Scores: 1.76e-295 Length: 7053
Pred. No.:

US-10-037-270-267
Sequence 267, Application US/10037270
Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhilwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
CURRENT APPLICATION NUMBER: US/10/037, 270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: PL FL_genes, Version 1.0
SEQ ID NO 267
LENGTH: 4942
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (186)..(3755)
US-10-037-270-267

Alignment Scores:
Pred. No.: 9,93e-16 Length: 4942
Score: 258.50 Matches: 109
Percent Similarity: 36.85% Conservative: 62
Best Local Similarity: 23.49% Mismatches: 136
Query Match: 8.41% Indels: 157
Gaps: 15

US-09-687-230A-2 (1-589) x US-10-037-270-267 (1-4942)

QY 11 AsplyshisileutyrgluyluValGluLysProLeuLysLeuValLeuLysValGly 30
Db 1341 GATGTTCACACGCTCCAGCGTGCACCCGAGGCTCTGAATATTTCGGGATGTC--- 1397
QY 31 GlyAsnGluValThrGluLeuSerThrGlySerSerGlyHisAspSerSerLeuPheGlu 50
Db 1398 -----GAAATGAAATAATGGCGTCTGTGAAAGAGAGCTCGTTAAACG 1442
QY 51 AsplyshisAspHisAspLysHisLysAspArgLysLysLysValGlyLysGlyGlu 70
Db 1443 GTCAAGTCC-----ACATCCAGCTCAGGAAGAGCAAAAAGGCTTAAG 1487
QY 71 Lys-----GlnLleProGly 75
Db 1488 AAGAGCTGTGCTGAGCCCTGCGGCTCTGCCGACCGTGCCTTATTATCCCCCG 1547
QY 76 GluGluLysGlyArgLysArgArgValLysGluAspLysLys----- 91
Db 1548 CAGAGGTTAAATAGATTGCCAATCAGGTGCGCATTCAGCGGAAGAGAGCTTTGTGAG 1607
QY 91 ----- 91

Db 1608 CGAGCCACAGTACTGCTGCTCAACGGGCTGTCCAGAAACGGGCCCCCTGCTCGG 1667
QY 92 -----ArgAspArgAspArgVal 97
Db 1668 CGGCTGAGTTCACGCTTCAGCTTCAGGAAAGCTCACAGACAGAAATGATGAGAG 1727
QY 98 GluAsnGluValGluLysAspLeuGlnCysHisLalProValArgLeuAspLeuProPro 117
Db 1728 ATGAGGCTCCCAAGAGAGAGCTGAATCTGGCAGCGGCTCGGCACGACCTGAGCCG 1787
QY 118 GluLysProLeuThrSerSerLeuAlaLysGln-----Glu 130
Db 1788 GCTCGCTGCTGATCCAGCTGTCCGACGGGAGAGCTCAAGCTGACAGAGTGAAG 1847
QY 131 ValGln-----ThrProLeuGlnGlnLalLeuAsnGln 143
Db 1848 GTGAGCAGGTCCCATGAGCTGCGGCTGACCCGCTGACGCTGCTGCGCTCAGTG 1907
QY 144 MetArgGlnLeuGlnArgLysAspProSerAlaPhePheSerPheProValThrAspPhe 163
Db 1908 CTGACCAAGCTGCAGACAGACAGCCGACAGATATTTCGACGCCCTGAGCTGAG 1967
QY 164 IleAlaProGlyTyrSerMetIleLysHisProMetAspPheSerThrMetLysGlu 183
Db 1968 GAGGTACCAAGATTATTGATCACAATTAACATCCCATGAGACTTGGCCAAATGAGAAA 2027
QY 184 LysIleLysAsnAspLysArgLysLysLysLysLysLysLysLysLysLysLysLys 203
Db 2028 CGGTTAGAACCTCAAGGATTAATAAACCTTCATGATGATGAGAGAGATTGATTCATT 2087
QY 204 CysThrAsnAlaMetIleTyrAsnLysProGlnThrIleTyrLysLysLysLysLys 223
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QY 224 LeuLeuHisSerGlyMetLysIleLeuSerGlnGluArgGlnGlnSerLeuLysGlnSer 243
Db 2148 CTCGCGCATCAGAGAGGTGTTGTTGTGAGGCGAGCCCG----- 2186
QY 244 IleAspPheMetAlaAspLeuGlnLysThrArgLysGlnLysAspGlyThrAspThrSer 263
Db 2186 ----- 2186
QY 264 GlnSerGlyGluAspGlyGlyCysTrpGlnArgGluAspSerGlyAspAlaGlu 283
Db 2187 -----CGGAGGTGACAGCATCGGCTTGGAAAG 2216
QY 284 Ala-----HisAlaPheLysSerProSerLysGluAsnLys----- 236
Db 2217 GCCTCGGCGATGACCTCGCTGAGCGGCTGTGCGGACCGGCGGCGCTTCTCTCG 2276
QY 297 LysAspLysAspPheLeuGluAspLysPheLysSerAsnAsnLeu-----GluArg 313
Db 2277 GAAGACGTGACAGGTGCTGAGACCCCGCCAAAGAGCCACCTGGGCTCGAGAGAGAG 2336
QY 314 GluGlnGlnGlnLeuAspArgLys-----ValLysGlnSerGlyLysLys 328
Db 2337 CTGAGAGCTGTGAGCATGCTGACCTGACCTGACCTGAGTGAAGTCAAGCGGCTCCGG 2396
QY 329 LeuThrArg-----ArgLeuValAsnSerGlnCysGluPheGlnArgLysProAspGly 347
Db 2397 AGCAAGCGGCAAGAGCTGCTCAAAAGAAATAGCCCTTCTCGAAACAG----- 2447
QY 348 ThrThrThrLeuGlnLeuLeuHisProValAspProLleValLysLysProGlyTyrCys 367
Db 2448 -----CTGAGCCAGACAGCAGC-----CAGCCCTGCGCCAGCGGCGCAGGC----- 2489
QY 368 LeuValArgLeuLysMetThrThrArgLysGlnSerGlyValAsnThrLeuGlnGly 387
Db 2490 -----TTGAAAGGC 2498
QY 388 PheLysGluAsp 391
Db 2499 TTCGAAGAGGAC 2510

RESULT 12
 US-10-109-886-9
 Sequence 9, Application US/10109886
 Publication No. US20020119499A1
 GENERAL INFORMATION:
 APPLICANT: TANABE SEIYAKU CO. LTD.
 APPLICANT: TANIGUCHI, Tomoyasu
 APPLICANT: MIKUMI, Junko
 TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND
 TITLE OF INVENTION: ANTAGONIST TO PPAR
 FILE REFERENCE: TANIGUCHI=6
 CURRENT APPLICATION NUMBER: US/10/109, 886
 PRIOR FILING DATE: 2002-04-01
 PRIOR APPLICATION NUMBER: 09/514,247
 PRIOR FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: PCT/JP98/03734
 PRIOR FILING DATE: 1998-08-24
 PRIOR APPLICATION NUMBER: JP231084/1997
 PRIOR FILING DATE: 1997-08-27
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 9
 LENGTH: 8147
 TYPE: DNA
 ORGANISM: human
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (819)..(8147)
 US-10-109-886-9

Alignment Scores:
 Pred. No.: 3,27e-12 Length: 8147
 Score: 227.00 Matches: 149
 Percent Similarity: 34.18% Conservative: 80
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 Query Match: 7.39% Indels: 227
 Gaps: 30

US-09-687-230A-2 (1-589) x US-10-109-886-9 (1-8147)
 QY 36 GluLeuSerThrGlySerSerGlyHisAspSerSerLeuPheGluAspLysAsnAsp--- 54
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 QY 55 -----HisAspLysHisLysAspArgLysArgLysLysLysLysGln 72
 Db 3822 CAAGCAGAGCAGCAGCAGCAGCAGT----- 3845
 QY 73 LLeProGlyGluGluLysGlyArgLysArgArgValLysGluAsp----- 88
 Db 3846 ---CCTGCTGATTCAGAAAGGAGAGCCAGCTCTGAGATGATGAGAGGATTTGCAAGGA 3902
 QY 89 -----LysLysLysLysAspArgAspArgValGluAsnGluValGluLysAspLysGln 106
 Db 3903 GCTTCCCAAGTTAAAGAAAGAAACAGACATACAGAGCAGAAATCAGAA----- 3950
 QY 107 CysHisAlaProValArgLysAspLeuProProGlyLysProLeuThrSerSerLeuAla 126
 Db 3951 -----CCAAATCGAAGTGGAT-----GAAAAGAAACCTGAAAGTGAAGTGAAGTT 3995
 QY 127 LysGlnGluGluValGluGlnThr----- 134
 Db 3996 AAAAGAGAAAGAGAGAGTAGCAGTAACGACAGCCTTCTCAATCTCTTCGCGAG 4055
 QY 135 -----ProLeuGlnGluAlaLeuAsnGlnLeuMetArg 145
 Db 4056 CCGGCGCAAAATCTTTAAACAGAGAGAGTAGTACGCCAGCCTCTCATCCCAACCTTGAA 4115
 QY 146 GlnLeuGlnArgLysAspProSerAlaPhe---PheSerPheProValThrAspPhe 164
 Db 4116 GCACGTATCGACAGAGCAGCAGAGATCACTTTCCGCGAGCCTGTAGATCCCGAGCTC 4175

QY 165 -----AlaProGlyTyrSerMetIleIleLysHisProMetAspPheSerThrMetLys 182
 Db 4176 CTCGGAATTCAGACATCTTTTGAACATGTAAAGATCCATGAGCCTCTCCACCATCAG 4235
 QY 183 GluLysIleLysAsnAspLysArgLysSerIleGluGluLeuLysAspAsnPheLysLeu 202
 Db 4236 CGAAGCTGACACAGGCAATCAAGACCCCTGGACAGACGTGACGACGTGCTC 4295
 QY 203 MetCysThrAsnAlaMetIleTyrAsnLysProGluThrIleTyrTyrLysAlaAlaLys 222
 Db 4296 ATGTTCACAAATGCTGCTGCTCTTAATCGCAAGACATCCGAGCTCTTAAGTTTGAC 4355
 QY 223 LysLeuLeuHisSerGlyMetLysIleLeuSerGlnGluArgIleGlnSerLeuLysGln 242
 Db 4356 AAGCTT-----GCAGAGCTTTGACAGAGAA---ATTGACCTGTGATCAG 4400
 QY 243 SerIleAspPheMetAla----- 248
 Db 4401 TCCCTTGATATTGCTGTGACGCAAGTAGTTTCCACAGACTTTGTGCTGCTAT 4460
 QY 249 AspLeuGlnLysThrArgLysGlnLysAspGlyThrAspThrSerGlnSerGlyLysAsp 268
 Db 4461 GGAAGCAGCTGTGTACCATTTCTCGGATGCTGCTCACTACAGCTTCAAGATAGGTAT 4520
 QY 269 GlyLysCys-----TyrGlnArgGluArgLysAspSerGlyAspAla 282
 Db 4521 CATTTCTGTAGAGAGTGTTCACAGAGATCCAGGCGAGAAATGACCTCGGGTAC--- 4577
 QY 283 GluAlaHisAlaPheLysSerProSerLysGluAsnLysLysLysAspLysAspMetLeu 302
 Db 4578 -----GACCTTCACAGCAGCCAGCAGCAGCAATTTCAAGAGATCAAGTTT 4619
 QY 303 GluAspLysPheLysSerAsnAsnLeuGlu----- 312
 Db 4620 GAAGAGAG---AAATATGATACCTTAGACCCGAACTTCTGTTGATTCAGAGAGTGT 4676
 QY 313 ---ArgGlnGlnGlnGlnLeu----- 318
 Db 4677 GGGCGAAGATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 4736
 QY 319 -----AspArgIleValLysGluSerGly----- 326
 Db 4737 GTGTGCACAACTGCTTGAAGAACTGCGCAGACTCGAAGAAAGAAACAAATTCAGTGT 4796
 QY 327 -----GlyLysLeuThrArgArgLysValAsnSerGlnCysGluPheGlu 341
 Db 4797 AAGAGCTGACAGACACAGACAGCTGGAAACCACTGGAGAGCAGAGTGAATTTTTC 4856
 QY 342 ArgArgLysProAspGlyThrThrThrLeuGlyLeuLeuHisAspProValAspProIleVal 361
 Db 4857 CGGCGCCAGAAAT-----CACCT----- 4874
 QY 362 GlyGluProGlyTyrCysLeuValArgLeuGlyMetThrThrArgLysGlnSerGly 381
 Db 4875 ---GAAGCCGGGAGAGTTTGTCCAGAGTGTGCGCAGCTCA----- 4913
 QY 382 ValAsnThrLeuGlnGlyPheLysGluAspLysArgAsnLysValThrProValLeu--- 400
 Db 4914 -----GACAAAGCGTGAAGGTCAAGCCGGGAGTAG 4946
 QY 401 -----TyrLeuAsnTyrGlyProTyrSerSerTyrAlaProHis---TyrAspSerThr 417
 Db 4947 TCACGTTTGTGATTTCTGGGAAATGTGATCTTTTCCATATGACAAAGCTCTG 5006
 QY 418 PheAlaAsnIleSerLysAspAspSerAspLeuIleTyr-----SerThr 432
 Db 5007 TTTCCTTTGAGCAAAATTGACGCGCTGATGCTGCTTTTGGAAATGACAGTCCAGAA 5066
 QY 433 TyrGlyGluAspSerAspLeuProSerAsp-----PheSer 444
 Db 5067 TACGGCTGTATGCCCCCTCCAAACAGAGCGGTGTGACATTTCTTATTCGTGATAGT 5126
 QY 445 IleHisGluPheLeuAlaThrCys-GlnAspTyrProTyrValMetAlaAspSerLeu 464

Db 5127 ATTCATTCTCCGCGCCAGCTGCTCCGACACCCGTTTACATGAGA---TCCTTATT 5183
Qy 464 UAPRVAL-----LeuThryLysGlyLysIserArgThrLeu 476
Db 5184 GGATATTGAGATGATGAGAAATTAGGATGTGACAGGGCACATCTGGGCTGTCT 5243
Qy 476 UGInGluMeGluMeSerLeuProGluAspGluGlyHis-----489
Db 5244 CCAAGTAGAGAGATGATTACATCTTCATTTGCCACCCACCTGATCAAAAATACCCAG 5303
Qy 490 -----ThryArgThryLeuAspThryGly 497
Db 5304 CCAAAACGACTGACAGAGTGGTACAAAAGATGCTGACAAAGCGTTTGCAGACGGATC 5363
Qy 497 sgluMeGlu-GlnIleThryGluValGluProGluArgLeuAspSer-ThryGln 516
Db 5364 ATCCATGACTACAA-----GGAATTATTTCAAAACAAAGCAACTGAA 5402
Qy 517 AspArgLeuIleAlaLeuLysAlaValThryAspPheGlyValProValGluValPheAsp 536
Db 5403 GACAGCTCACACGACGCGCAAGAACTGCCCTATT-----5438
Qy 537 SerGluGluAlaGluIlePheGlnLysLeuAspGluThrThryArgLeuArgGlu 556
Db 5439 -----GAGGTGATTCTGGCCCAATGTGTAGAGAGAC-----ATTAAGAA 5483
Qy 557 LeuGlnGluAlaGlnAsnGluArg 564
Db 5484 CTAGAACAAAGAAAGAGAGAGG 5507

RESULT 13
US-09-925-301-104
; Sequence 104, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-104

Alignment Scores:
Pred. No.: 2,01e-12 Length: 1636
Score: 219.50 Matches: 75
Percent Similarity: 48.30% Conservative: 53
Best Local Similarity: 28.30% Mismatches: 94
Query Match: 7.14% Indels: 44
DB: 9 Gaps: 11

US-09-687-230A-2 (1-589) x US-09-925-301-104 (1-1636)

Qy 323 LysGluSerGlyLysLeuThryArgArgLeuValAsnSerGlnCysGluPheGluArg 342
Db 40 GAGGACGGGACGCGACCTGCTCTACAGCGTGTCAACGCGCC-----GACCGA 90
Qy 343 ArgLysProAspGlyThrThryLeuGlyLeuLeuHisProValAspProIleValGly 362
Db 91 CGCGTAGAGAGAGA-----GACCA-----111
Qy 363 GluProGlyThryCysLeuValArgLeuGlyMetThryGlyArgLeuGlnSerGlyVal 382

Db 112 ---CCGGT-----GACTTGAGCTCGCTCTCCAGTAAGCTACTCCAGGCTTC 156
Qy 383 AsnThryLeuGlnGlyPheLysGluAspLysArgAsnLysValThryProValLeuThryLeu 402
Db 157 ACCAGCTG---GGCTTCAAAGACGAGAGAAAGAAAGAACTACCC-----TTCTC 204
Qy 403 AsnThryGlyProThrySerLeuThryAlaProHisLeuThryAspSerThryPheAlaAsnIleSer 422
Db 205 TCC---AGTGCACACTACTGCGCTTTCGATGACAAATPATTCAATATTGGCGACTTGAAG 261
Qy 423 LysAspAspSerAspLeuIleThrySerThryGlyGluAspSerAspLeuProSerAsp 442
Db 262 TCCGACGAGATGAGTGGCTCTCTACTCAGCTTACGAGATAGACAGCGCTGAGTGGC 321
Qy 443 PheSerIleHisGluPheLeuAlaThryCysGluAspThryProThryValMetAlaAspSer 462
Db 322 CTGAGCTGCGAGAGTGTGAGAGATGCTGGAGCTACAGCAAGAAAGTGTGGAGAC 381
Qy 463 LeuLeuAspValLeuThryLysGlyGlyHisSerArgThryLeuGlnGluMeGlu-----480
Db 382 CTCCTGACCAATACACAGCGGAGACCACTTACGACGCTCTTCCAGCTGAAGCAGAGA 441
Qy 481 -----MetSerLeuProGluAspGluGlyHisThryArgThryLeu---AspThr 495
Db 442 AGAAATGTTCCCATGAAGCTCCAGATGAAGCAAGTTGGGAGACCCCTAGAGACAGC 501
Qy 496 GlyLysGluMeGluGlnIleThryGluValGluProGluArgLeuAspSerThry 515
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Qy 536 AspSerGluGluAlaGluIlePheGlnLysLeuAspGluThrThryArgLeuLeuArg 555
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Qy 556 GluLeuGlnGluAlaGlnAsnGluArgLeuSerThryArgProProGluAsnMetIleCys 575
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RESULT 14
US-09-864-761-11927
; Sequence 11927, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11927
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC016498.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
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; US-09-684-761-11927

Alignment Scores:
Pred. No.: 1,2e-12 Length: 577
Score: 215.50 Matches: 44
Percent Similarity: 78.31% Conservative: 21
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QY 30 GlyGlyAsnGluValThrGluLeuSerThrGlySerSerGlyHisAspSerSerLeuPhe 49
DB 143 GGAGGAAGTGAAGTGAAGTGAAGTCA-----GGATCCGGCCAGCACTCCAGTTACTAT 196
QY 50 GluAspLysAsnAspHis-----AspLysHisAspArgLysArgLysLysArgLys 67
DB 197 GATGACAGTCAAGACATGAGAGAGAGAGAGCAAAAGAAAAGAAAGAGAGAGAG 256
QY 68 LysGlyGluLysGluHisProGlyGluGluLysGlyArgLysArgArgValLysGlu 87
DB 257 AAGTCCGAGAGAGAGAGAGAGATCTGACATGAGAGAGAGAGAGAGAGAGAGAG 316
QY 88 AspLysLys 90
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RESULT 15
US-09-764-887-619
; Sequence 619, Application US/09764887
; Patent No. US2002042096A1
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P413
; CURRENT APPLICATION NUMBER: US/09/764,887
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 619
; LENGTH: 32222
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-887-619

Alignment Scores:
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Score: 215.50 Matches: 44
Percent Similarity: 78.31% Conservative: 21
Best Local Similarity: 53.01% Mismatches: 9
Query Match: 7.01% Indels: 9
DB: 9 Gaps: 3

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QY 30 GlyGlyAsnGluValThrGluLeuSerThrGlySerSerGlyHisAspSerSerLeuPhe 49
DB 25058 GAGGAAGTGAAGTGAAGTGAAGTCA-----GGATCCGGCCAGCACTCCAGTTACTAT 25111
QY 50 GluAspLysAsnAspHis-----AspLysHisAspArgLysArgLysLysArgLys 67
DB 25112 GATGACAGTCAAGACATGAGAGAGAGAGAGCAAAAGAAAAGAAAGAGAGAG 25171
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Job time : 515 secs
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GenCore version 5.1.6
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
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5: /cg2_6/ptodata/2/ina/PTCUS.COMB.seq.*
6: /cg2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	745	24.2	477	4	US-08-747-562-29
3	258.5	8.4	4549	4	US-09-620-312D-266
4	258.5	8.4	4942	4	US-09-620-312D-267
5	227	7.4	8147	4	US-09-514-247A-9
6	205	6.7	7326	4	US-08-194-468-1
7	205	6.7	7326	4	US-08-514-247A-7
8	205	6.7	7344	3	US-08-961-739-1
9	198	6.4	2330	2	US-08-557-128-3
10	198	6.4	2330	3	US-08-557-128-3
11	192.5	6.3	5477	4	US-09-242-690A-34
12	191	6.2	5480	4	US-09-535-008-74

13	191	6.2	5564	4	US-09-535-008-68	Sequence 68, Appl
14	190.5	6.2	9046	1	US-08-227-536-1	Sequence 1, Appl
15	190.5	6.2	9046	5	PCT-US95-04682-1	Sequence 1, Appl
16	189.5	6.2	5567	4	US-09-535-008-64	Sequence 64, Appl
17	188.5	6.1	5468	4	US-09-535-008-66	Sequence 66, Appl
18	188.5	6.1	5573	4	US-09-535-008-76	Sequence 76, Appl
19	187	6.1	5386	4	US-09-535-008-60	Sequence 60, Appl
20	187	6.1	5471	4	US-09-535-008-1	Sequence 1, Appl
21	187	6.1	5471	4	US-09-535-008-62	Sequence 62, Appl
22	187	6.1	5576	4	US-09-535-008-72	Sequence 72, Appl
23	181.5	5.9	5962	1	US-08-188-582-10	Sequence 10, Appl
24	181.5	5.9	5962	1	US-08-646-715-10	Sequence 10, Appl
25	170.5	5.5	4164	1	US-08-188-582-3	Sequence 3, Appl
26	170.5	5.5	4164	1	US-08-646-715-3	Sequence 3, Appl
27	159	5.2	6755	3	US-08-931-999-4	Sequence 4, Appl
28	154	5.0	8789	1	US-08-328-254-5	Sequence 5, Appl
29	153	5.0	3104	4	US-09-418-780A-2	Sequence 2, Appl
30	151	4.9	4868	5	US-08-139-937-12	Sequence 12, Appl
31	151	4.9	4868	5	PCT-US93-11310-12	Sequence 12, Appl
32	150.5	4.9	5893	2	US-08-687-080-44	Sequence 44, Appl
33	150	4.9	5661	4	US-08-938-105-2	Sequence 2, Appl
34	149.5	4.9	5893	1	US-08-592-126-54	Sequence 54, Appl
35	149.5	4.9	5893	4	US-09-168-595-54	Sequence 54, Appl
36	147.5	4.8	4766	5	PCT-US93-07261-10	Sequence 10, Appl
37	147	4.8	9551	1	US-08-056-200-93	Sequence 93, Appl
38	147	4.8	9551	2	US-08-800-644-93	Sequence 93, Appl
39	146.5	4.8	4882	4	US-09-620-312D-1065	Sequence 1065, Ap
40	145.5	4.7	8257	4	US-09-595-684B-30	Sequence 30, Appl
41	145.5	4.7	8503	4	US-09-620-312D-130	Sequence 130, App
42	144	4.7	2527	4	US-09-555-790A-1	Sequence 1, Appl
43	142	4.6	6773	4	US-09-166-350-27	Sequence 27, Appl
44	142	4.6	10136	1	US-08-353-700-2	Sequence 2, Appl
45	142	4.6	10136	5	PCT-US95-16216-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-942-008-1
Sequence 1, Application US/08942008
Patent No. 6133419
GENERAL INFORMATION:
APPLICANT: Baezelmann, Sylvia
TITLE OF INVENTION: Nucleotide Sequences that Encode
Phosphatidylinositol-3' Kinase Associated Proteins and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: CA
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,008
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX1027
TELEPHONE: (510) 262-8710
TELEFAX: (510) 222-9758
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2307 base pairs


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QY 31 GlyAsnGluValThrGluLeuSerThrGlySerSerGlyHisAspSerSerLeuPheGlu 50
Db 1398 -----GAAATCAAAAATGGCTCTGTGCAAAAAGAGAGCTCGGTATTAACG 1442
QY 51 AspLysAsnAspHisAspLysHisLysAspArgLysLysArgLysLysGlyGlu 70
Db 1443 GTCAAGTCC-----ACATCCAAAGGTCAAGAAAGGCAAAAAGAGGCTTAAG 1487
QY 71 Lys-----GlnIleProGly 75
Db 1488 AAGACTGTGCTGAGCCCTGGCGGCTCTGCGAACCTGTGCGCTCTTATATATCCCGC 1547
QY 76 GluGluLysGlyArgLysArgArgValLysGluAspLysLysLys----- 91
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QY 98 GluAsnGluValGluLysAspLeuGlnCysHisAlaProValArgLeuAspLeuProPro 117
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QY 118 GluLysProLeuThrSerSerLeuAlaLysGlnLys-----Glu 130
Db 1788 GCTGCGCTGCTGATCGAGCTCTGCGGAGGAGGAAAGCTCAAGCTGAGCAGGTAG 1847
QY 131 ValGluGln-----ThrProLeuGlnGluAlaLeuAsnGlnLeu 143
Db 1848 GTGAGAGCGGTGCGCATGAGAGCTGCGGCTGAGCGGTGCTGCTGCTGCTGCTG 1907
QY 144 MetArgGlnLeuGlnArgLysAspProSerAlaPheSerPheProValThrAspPhe 163
Db 1908 CTGAGCAGCTGCGAAGACAGAGAGAGAGAGAGAGATTTGGCGAGCCCTGATGCTG 1967
QY 164 IleAlaProGlyTyrSerMetIleLysHisProMetAspPheSerThrMetLysGlu 183
Db 1968 GAGTACCAAGATTTATGGATCACTTAACTCCATCCAGGACTTTGCCACATAGAGAA 2027
QY 184 LysIleLysAsnAsnAspTyrGlnSerIleGluGluLeuLysAspAsnPheLysLeuMet 203
Db 2028 CGGTAGAGAGCTCAAGCGTATTAACCTCATGATGTTGAGAGAGATTTGATCTCAT 2087
QY 204 CysThrAsnAlaMetIleTyrAsnLysProGluThrIleTyrTyrLysAlaAlaLysLys 223
Db 2088 ATGATTAATCTGATTAAGTACAAATGCCAGGAGACCGTGTCTTATAGAGCGGCTG 2147
QY 224 LeuLeuHisSerGlyMetLysIleLeuSerGlnGluValGlnSerLeuLysGlnSer 243
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QY 244 IleAspPheMetAlaAspLeuGlnLysThrArgLysGlnLysAspGlyThrAspThrSer 263
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QY 284 Ala-----HisAlaPheLysSerProSerLysGluAsnLysLys----- 296
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QY 297 LysAspLysAspMetLeuGluAspLysPheLysSerAsnAsnLeu-----GluArg 313
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QY 314 GluGlnGluGlnLeuAspArgIle-----ValLysGlnSerGlyLys 328
Db 2337 CTGAGAGAGCTGCTGAGCATGCTGCACTCACTGCGGCTATGAGTCAAGCGGCTCCCG 2396
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QY 348 ThrThrThrLeuGlyLeuLeuHisProValAspProIleValGlyGluProGlyTyrCys 367
Db 2448 -----CTGAGCCAGCAGCAGCAGC---CAGCCCTGCGCCAGGCGCAGC----- 2489
QY 368 LeuValArgLeuGlyMetThrThrGlyArgLeuGlnSerGlyValAsnThrLeuGlnGly 387
Db 2490 -----TTGGAAGGC 2498
QY 388 PheLysGluAsp 391
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RESULT 4

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US-09-620-312D-267
: Sequence 267, Application US/09620312D
: Patent No. 6569662
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Xuendi, Yindod
: APPLICANT: Zhang, Jie
: APPLICANT: Ren, Feiyan
: APPLICANT: Chen, Rui-hong
: APPLICANT: Zhao, Qing A.
: APPLICANT: Wehrman, Tom
: APPLICANT: Xue, Aidong J.
: APPLICANT: Yang, Yonghong
: APPLICANT: Wang, Jiao-Rui
: APPLICANT: Zhou, Ping
: APPLICANT: Ma, Yundong
: APPLICANT: Wang, Dunhui
: APPLICANT: Wang, Zhiwei
: APPLICANT: John Tillinghast
: APPLICANT: Drmanac, Radjoje T.
: TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
: FILE REFERENCE: 784C1P28
: CURRENT APPLICATION NUMBER: US/09/620,312D
: CURRENT FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: 09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: 09/488,725
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 1105
: SOFTWARE: pc_fl_genes Version 1.0
: SEQ ID NO 267
: LENGTH: 4942
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (186)..(3755)
US-09-620-312D-267

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Alignment Scores:

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Pred. No.: 7.03e-18 Length: 4942
Score: 258.50 Matches: 109
Percent Similarity: 36.85% Conservative: 62
Best Local Similarity: 23.49% Mismatches: 136
Query Match: 8.41% Indels: 157
DB: 4 Gaps: 15

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Qy 71 Lys-----GlnLeuProGly 75
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Qy 91 ----- 91
Db 1608 CAGAGCCACAGCTACTGCTGCTCAGAGCGCTGTCAGAGAGAGAGAGAGAGAG 1667
Qy 92 -----ArgAspArgAspArgVal 97
Db 1668 CGGCTGAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 1727
Qy 98 G1uAsnGluValGlyValAspLeuGlnCysHisAlaProValArgLeuAspLeuPro 117
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Db 2397 AGCAGCGGAGAGAGCTGCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2447
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Qy 368 LeuValArgLeuGlyMetThrThrArgValArgLeuGlnSerGlyValAlaThrThr 387
Db 2490 -----TTGAGAGGC 2498
Qy 388 PheLysGluAsp 391
Db 2499 TTGAGAGAGAGAG 2510
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US-09-514-247A-9
Sequence 9, Application US/09514247A
Patent No. 6353361
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
FILE REFERENCE: TANIGUCHI-6
CURRENT APPLICATION NUMBER: US/09/514, 247A
CURRENT FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 8147
TYPE: DNA
ORGANISM: human
FEATURES:
NAME/KEY: CDS
LOCATION: (819)..(8147)
US-09-514-247A-9
Alignment Scores:
Pred. No.: 4.8e-14 Length: 8147
Score: 227.00 Matches: 149
Percent Similarity: 34.18% Conservative: 80
Best Local Similarity: 22.24% Mismatches: 214
Query Match: 7.39% Indels: 227
DB: 4 Gaps: 30
US-09-687-230A-2 (1-589) x US-09-514-247A-9 (1-8147)
Qy 36 G1uLeuSerThrGlySerSerGlyHisAspSerSerLeuPheGluAspAsp--- 54
Db 3762 GAAACCAATTCACAG 3821
Qy 55 -----HisAspLysHisAspArgValArgValArgValArgValArgValArg 72
Db 3822 CAGCAG 3845
Qy 73 IleProGlyGluGluGlyValArgValArgValArgValArgValArgValArgVal 88
Db 3846 -----CTGTGTGAATCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3902
Qy 89 -----LysLysLysArgAspArgValGluAsnGluLysLysLysLysLysLys 106
Db ----- 106


```

1 CLING DATE: 10-FEB-1994
2 CLASSIFICATION: 435
3 ATTORNEY/AGENT INFORMATION:
4
5 NAME: Reiter, Stephen E.
6 REGISTRATION NUMBER: 31,192
7 REFERENCE/DOCKET NUMBER: P41 96722
8 TELECOMMUNICATION INFORMATION:
9
10 TELEPHONE: (619)-546-4737
11 TELEFAX: (619)-546-9392
12
13 INFORMATION FOR SEQ ID NO: 1:
14
15 SEQUENCE CHARACTERISTICS:
16
17 LENGTH: 7326 base pairs
18 TYPE: nucleic acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21
22 MOLECULE TYPE: DNA (genomic)
23
24 HYPOTHEetical: NO
25
26 ANTI-SENSE: NO
27
28 FEATURE:
29
30 NAME/KEY: CDS
31 LOCATION: 1..7323
32
33 US-08-194-468-1

```



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Db      3967 AACAAATTCAGTCTAAGAGGCTGACAGACCAAGATTGGAAACCACTTAAGAGACAGA 4026
Qy      337 GlnCysgluPheGluAsgArglyLeuProArglyThrThrLeuGluLeuLeuHisPro 356
Db      4027 GTGAATAGATTTTGGCGCGCAGAAAT-----CACCCCT 4059
Qy      357 ValAspProIleValGluProGlyTyrCysLeuValArgLeu----- 371
Db      4060 -----GAAAGCTGGGAGGTTTGTCTCAGAGTGGGCGCAGCTCAGAC 4101
Qy      372 -----GlyMetThrThrGlyArgLeuGlnSerGly----- 381
Db      4102 AAGACTGTGAGGTCAAGCCGGAATGAAGTGAAGTTTGATCTCGAGAGATGTGCG 4161
Qy      382 -----ValAspThrLeuGlnGlyPheLeuGlu----- 390
Db      4162 GAATCTTTCCCATATGCTACCAAGACACTCTTGTCTTGAAGAGATGATGAGTGCAT 4221
Qy      391 -----AspLysArgAsnLysValThr 397
Db      4222 GTGTGCTTTTGGATGCATGTGCAAGATACGCTGTGATGCCCCCAAAATACAA 4281
Qy      398 ProValLeuTyrLeuAsnTyr-GlyProTyrSerSerTyrAla----- 411
Db      4282 GGGTGTGTATACATATCTTATCTGACAGATTCATTCTTCGGCGCGCTGCTCGG 4341
Qy      412 -----ProHis-----T 414
Db      4342 ACAGCTGTTTACCATGAGATCTCTCATGATCTCGATATCTGAAGAAATGGTAT 4401
Qy      414 YrsAspSerThrPheAlaAsnIleSer---Lys-AspAspSerAspLeuIleTyrSerThr 432
Db      4402 GTACACGACATATTTGGCGCTGTCTCCCAAGTGAAGAGATGACTATATCTTTCATGCG 4461
Qy      433 TyrGlyGluAspSerAspLeuProSerAspPheSerIleHisGluPheLeuAlaThrCys 452
Db      4462 CACCCCGCTGACCAAGAAATCCCAACCAAGAAAGACTACAGAGAGTGTCAAGAAAGATG 4521
Qy      453 GlnAspTyrProTyrVal-----MetAlaAspSerLeuLeuAspValLeuThrLysGly 470
Db      4522 CTCGACAGGCGCTTTCGACAGAGATCATTAACGACTATGAAGACATCTTCAAAACAGCG 4581
Qy      471 GlyHisSerArgThrLeuGlnGluMetSerLeuProGluAspGluGlyHisThr 480
Db      4582 AACGAAGACAGGCTCAGAGTCCCAAGAGTGTCCCTATTTGAAGAGATTTCTGGCCT 4641
Qy      491 ArgThrLeuAspThrGly---LysGluMetGluGlnIleThrGluValGluProGly 509
Db      4642 AATGTGTGGAAGAAAGCACTTAAGAACTAGAACAA-----GAAGAAAGAAAGAAAGAA 4695
Qy      510 ArgLeuAspSerSerThrGlnAsp-ArgLeuIleAlaLeuLysAlaValThrAsnPheG 529
Db      4696 AAGAAGAGAGGTACTCAGCGAGTGAAGTCTCTGAGGCGCAGTCAAGGTGACA----- 4747
Qy      529 yValProValGluValPheAspSerGluGluIleGluIlePheGlnLysLysLeuAspG 549
Db      4748 -----GCAAAATATCGAAGAAAGAA----- 4768
Qy      549 uThrThrArg-----LeuLeu-ArgGluLeuGlnGluAlaG 561
Db      4769 -ACAACAAAGAAAGCAAAACAAACAAAGACATTTAGCCGCCCAACAAAGAAAGAGCCC 4827
Qy      561 IlnAsnGluArgLeuSerThrArgProProGlyLysAsnMetIleCys 575
Db      4828 AGCATGCCCAATGTTTCAACGACCTGTGCGAAGAGCTGTATGC 4871

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; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/08/961,739A
; CURRENT FILING DATE: 1997-10-31
; EARLIER APPLICATION NUMBER: US 194,468
; EARLIER FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7326
; TYPE: DNA
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) (7326)
; NAME/KEY: misc_feature
; LOCATION: (1) (7326)
; OTHER INFORMATION: n = A,T,C or G
US-08-961-739-1

Alignment Scores:
Pred. No.      1.1e-11      Length:      7344
Score:         205.00      Matches:     150
Percent Similarity: 34.26%      Conservative: 96
Best Local Similarity: 20.89%      Mismatches:  237
Query Match:    6.67%      Indels:     235
DB:             3          Gaps:         30

US-09-687-230A-2 (1-589) x US-08-961-739-1 (1-7344)
Qy      32 AsnGluValThrGluLeuSerThrGlySerSerGlyHisAspSerSerLeuPheGluAsp 51
Db      2911 AATAGATCTCTTAATCTCCCTGCACTGTGACCAAGTCTGAAACCGATTCC-----CAGCAG 2964
Qy      52 LysAsnAspHisAspLysHisLysAspArgLysArgLysArgLysArgLysArgLysGly 71
Db      2965 CCAGACCCGAGTGTGCCATGCTCGAATGAAGACAGAGGTGCAGACATGATGTGTGAG 3024
Qy      72 GlnIleProGlyGluGluLysGlyArgLysArgLysArgLysValLysGluAsp----- 88
Db      3025 CCTGAACCTACTGAATCCCAAGGGGAACTCGGTCTGAATGATGGAAGGATTTCACAA 3084
Qy      89 -----LysLysLysArgAspArgAspArgValGluAsnGluAlaGluLysAspLeu 105
Db      3085 GGTCTTCCCAAGTAAAGAAAGACAGATACGACAGACAGACAGAGTCAAGAGCA----- 3138
Qy      106 GlnCysHisAlaProValArgLeuAspLeuProProGlyLysProLeuThrSerSerLeu 125
Db      3139 -----ATGGAAGTAAAGAAAGAAAGAAACCTGAAGTAAAGTGCAGAA 3177
Qy      126 AlaLysGlnGluGluValGluGlnThr----- 134
Db      3178 GCTAAAGAGAAAGAAAGAAAGAGAGTTCGAACGACACAGCTCAATCAACATCTCTCC 3237
Qy      135 -----ProLeuGlnGluAlaLeuAsnGlnLeuMet 144
Db      3238 CAGCCAGCGCAAAATCTTTAAACCCGAGAGCTACGCGCAGCACTTATGCCCACTTCA 3297
Qy      145 ArgGlnLeuGlnArgLysAspProSerAlaPhe---PheSerPheProValThrAspPhe 163
Db      3298 GAAGCACTTATCTGACAGAGCCCAAGTCTTTGGCTTTTCGTGAGCTGTAGTCTCTCAAG 3357
Qy      164 Ile-----AlaProGlyTyrSerMetIleIleLysHisProMetAspPheSerThrMet 181
Db      3358 CTCCTAGGAATCCCAAGATTAATTTGATATAGGAAGAAATCCATAGGACCTTCTTCAACATC 3417
Qy      182 LysGluLysIleLysAsnAsnAspTyrGlnSerIleGluGlnLeuLysAsnAsnPheLys 201
Db      3418 AAACGAAGCTGACACAGAGGCAATATCAAGAACCTTGCAATATGTGATGTGATGTCAAG 3477
Qy      202 LeuMetCysThrAsnAlaMetIleTyrAsnLysProGluThrIleTyrTyrLysAlaAla 221
Db      3478 CTTATGTTCAACAAATCGGTGCTATTAATCGTAAAGCTCCCGTGTATTAATTTTGC 3537

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RESULT 8
US-08-961-739-1
; Sequence 1, Application US/08961739A
; Patent No. 6063583
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.

```

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Qy      222 LysLeuLeuHisSerGlyMetLysIleLeuSerGlnGluArgIleGlnSerLeuLys 241
      |||
      3538 AGTAACCTT-----GCAGAGCTTTTGAACAGAA---ATTGACCTGTCATG 3582
Qy      242 GlnSerIleAspMetAlaAspLeuGlnLysThrArgLysGlnLysAspGlyThrAsp 261
      |||
      3583 CAGTCTCTTGATATTCCTGTGCA-----CGAAAGTATGAGTTCTCCCAAG 3630
Qy      262 Thr----- 262
      |||
      3631 ACTTTGCTGTACGGAAGACAGCTGTATCAATTCCTGATGACGCTACTACAGC 3690
Qy      263 -----SerGlnSerGlyLysAspGlyLysTrp-----GlnArgGluArgGlu 277
      |||
      3691 TATCAGATATGATCATTTCTGTGGAGGTTCACAGATCCAGGCGGAGAAATGTG 3750
Qy      278 AspSerGlyAspAlaGluAlaHisAlaPheLysSerProSerLysGluAsnLysLys 297
      |||
      3751 ACCCTGGTAC-----GACCTTCCCACTCAGACGACAAATT 3789
Qy      298 AspLysAspMetLeuGlnLysLysPheLysSerAsnAsnLeuLys----- 312
      |||
      3790 TCCAGGATCATTTGAAAAGAG---AAAATGATACCTTAGATCTGAACCTTTGTT 3846
Qy      313 -----ArgGlnGlnGlnGlnLys----- 318
      |||
      3847 GACTGCAGAAAGTGTGCGGAGAGATGATCATGATTTGTTTACATGATCATATT 3906
Qy      319 -----AspArgIleValLysGlnSerGly----- 326
      |||
      3907 TGGCTTCAGGTTTGTGTGTGACACTGTTTGAAAGAAACTGACAGACCTCGGAAAGAA 3966
Qy      327 -----GlyLysLeuThrArgArgLeuValAsnSer 336
      |||
      3967 AACAAATTCACTGCTAAGAGCTGCAGACCAACAGATTGGAAACCTTAGAAGACGA 4026
Qy      337 GlnCysGluPheGluArgLysPheAspGlyThrThrLeuGlyLeuLeuHisPro 356
      |||
      4027 GTGAATTAAGTTTTCGCGCGCAGAAAT-----CACCTT 4059
Qy      357 ValAspProIleValGlyLysProGlyTyrCysLeuValArgLeu----- 371
      |||
      4060 -----GAGCTGGGAGGCTTTTGTCAAGTGTGCGACAGCTCAGAC 4101
Qy      372 -----GlyMetThrThrGlyArgLeuGlnSerGly----- 381
      |||
      4102 AAGACTGTGAGGTCAGACCGGAGATGAAGTCAGATTGTGAGATGTCG 4161
Qy      382 -----ValAsnThrLeuGlnLysPheLysGlu----- 390
      |||
      4162 GAATCTTCCATATTCATCCAAAGCACTTTGCTTTTGAGGAGATGATGAGTCAT 4221
Qy      391 -----AspLysArgAsnLysValThr 397
      |||
      4222 GTGCTTTTGGAGTCATGTCAGATACGCTGATGTCGCCCCCAACAAATACAA 4281
Qy      398 ProValLeuLysLeuAsnLysLysLysProLysSerSerLysAla----- 411
      |||
      4282 GCGTGTATATCATATCTTATCTGACAGTATTCATTTCCGCGCCGCTCCGG 4341
Qy      412 -----ProHis-----T 414
      |||
      4342 ACACGTGTTTACATGATGATCTCATCGATATCTCGATATGTGAAGAAATGGTGTAT 4401
Qy      414 TyrAspSerThrPheAlaAsnLysSer---Lys-AspAspSerAspLeuIleLysSerThr 432
      |||
      4402 GTGACAGACATATTGGGCGCTGTCCCAAGTGAAGAGATGACTATATCTTCATTGC 4461
Qy      433 TyrGlyLysAspSerAspLysProSerAspPheSerIleHisGluPheLeuAlaThrCys 452
      |||
      4462 CACCCCTGACAGAAATCCCAACCAACCAAGCACTACAGAGTGTGTACAGAAAGTG 4521

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Qy      453 GlnAspTyrProTyrVal-----MetAlaAspSerLeuLeuAspValLeuThrLysGly 470
      |||
      4522 CTGGACAGAGCGTTTCCAGAGAGATCATTAACGATATTAAGACATCTTCAAAAGCG 4581
Qy      471 GlyHisSerArgThrLeuGlnGlnLysMetGlnMetSerLeuProGluAspGlyHisThr 490
      |||
      4582 AACGAACAGAGCGTCAAGAGTGCAGAGTGCAGAGTGCCTATTTTGAAGAGATTTCTGCGCT 4641
Qy      491 ArgThrLeuAspPheLysLysLysLysGlnGlnLysIleThrGluValGluProGly 509
      |||
      4642 AATGTGTGAAGAAACATTAAGAACTTAGAAC-----GAGAGAGAAAGAAAGAA 4695
Qy      510 ArgLeuAspSerSerThrGlnLysPheArgLeuIleAlaLeuLysValThrAsnPheGln 529
      |||
      4696 AAGGAAGAGAGTCTCGACAGAGTGAATCTCCGAGGCGAGTCAGGCTGACA----- 4747
Qy      529 yValProValGluValPheAspSerGlnGluIlePheGlnLysLysLeuAspGln 549
      |||
      4748 -----GCMAAATGCCAAGAAAGAA----- 4768
Qy      549 uThrThrArg-----LeuLeu-ArgGluLeuGlnGluValag 561
      |||
      4769 -ACAAAGAAAGAACCAACAAACAAAGACAGCATTAAGCCGCGCAACAAAGAAAGCCC 4827
Qy      561 LysAsnGluArgLeuSerThrArgProProGlyAsnMetLysCys 575
      |||
      4828 AGCATGCCCAATGTTTCCAAAGCAAGCTGTGCGCAAGACTGATATC 4871

```

RESULT 9
 US-08-557-128-3
 ; Sequence 3, Application US/08557128
 ; Patent No. 5849524
 ; GENERAL INFORMATION:
 ; APPLICANT: KONDO, Keiji
 ; APPLICANT: KAJIWARA, Susumu
 ; APPLICANT: MISAWA, No. 5849524, Iiko
 ; TITLE OF INVENTION: TRANSFORMATION SYSTEMS FOR THE YEAST
 ; TITLE OF INVENTION: CANDIDA UTILIS AND THE EXPRESSION OF HETEROLOGOUS GENES
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/557,128
 ; FILING DATE: 25-JAN-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/JP95/01005
 ; FILING DATE: 25-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7-129287
 ; FILING DATE: 28-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-285823
 ; FILING DATE: 26-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-135015
 ; FILING DATE: 25-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 49441/108
 ; TELECOMMUNICATION INFORMATION:


```

Db      283 GAGGCGAGAGAAAGAGCA-----GAGAAAGAG-----309
Qy      124 SerLeuAlaLysGlnGluGluValGluGlnThrPro-----Leu 136
Db      310 -----GCAAGACCAAGAGGAGGAGAAAGAGCTCCGCTCCAGTCCGCAAGAGAGACTA 363
Qy      137 GlnGluAlaLeuGlnGlnLeuMetArgGlnLeuGlnArgLysAspProSerAlaPhePhe 156
Db      364 CAACACATTGCTACTCTCTCATCGAGAGCATCTCGTACATCAAGATACGCTCAGCGCTT 423
Qy      157 SerPheProValThrAspPheIleAlaProGlyTyrSerMetIleIleLysHisProMet 176
Db      424 CTACACCTCTTTAAGCATGATCCAGAGGACCAACATTAATCTCTGATCAAGAAACCAAG 483
Qy      177 AspPheSerThrMetLysGluLysIleLysAsnAsnAspTyrGlnSerIleGluGluLeu 196
Db      484 GATCTGAAAGACCAATCAACAGATGCTCAGAGACGAGCATATACAGACCAATCTTGACCTG 543
Qy      197 LysAspAsnThrLysLeuMetCysThrAsnAlaMetIleTyrAsnLysProGluThrIle 216
Db      544 GAGAGGAGATCTTGCTGATGTTTGGCAATGCCATCATGACACAGACCGGAGCGAT 603
Qy      217 TyrTyr-----LysAlaAlaLysLysLeuLeuHisSerGlyMetLysIle 232
Db      604 ATCTACAGATGAGACCAAGAGATGACCGGAACTTGAACAAGCTCATCGAGCTTTAAC 663
Qy      232 uSerGlnGluArgIleGlnSerLeuLysGlnSerIleAspPheMetAlaAspLeuGlnLys 252
Db      664 GAGAGTAATATGATATACAGCTTACAGATCAAAAGAGATGAAACAGCTCGATTAACG 723
Qy      252 gThrArgLysGlnLysAspGlyThrAspThrSerGlnSerGlyLysGlyCysTr 272
Db      724 GTATTGTAA-----TG 735
Qy      272 pGlnArgLysGlnLysAspSerGlyAspAlaGluAlaHisIleAspLysSerProSer-- 291
Db      736 GTATGTACAAAGGGGTGTCTTCTTCTCAACCTCTTTCATGTGTGAGTCAAAAGCAGCT 795
Qy      292 -----LysGluAlaLysLysLysAspLysAspMetLeuGlnAspLysPheLysSer 308
Db      796 TCTGCTCTTGAATCTAATCAAGACGACTCTTCCGAATCTTGAGAACTTTTCAAGAGCA 853

RESULT 11
US-09-535-008-74
; Sequence 74, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 5477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(5021)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1780)
; OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
; OTHER INFORMATION: position (position 1784 in GenBank) rather than
; OTHER INFORMATION: the G shown here.

```

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; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)
; OTHER INFORMATION: Polymorphism of either T or C in this noncoding
; OTHER INFORMATION: region.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1583)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1598)
; OTHER INFORMATION: Polymorphism of T or C resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1892)
; OTHER INFORMATION: Polymorphism of A or G resulting in a silent
; OTHER INFORMATION: mutation.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1445)..(1453)
; OTHER INFORMATION: Insertion of 9 basepairs as compared to SEQ ID
; OTHER INFORMATION: NO:1.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4507)..(4508)
; OTHER INFORMATION: Deletion of CNG between these basepairs as
; OTHER INFORMATION: compared to SEQ ID NO:1 (basepairs 4499-4501 of
; OTHER INFORMATION: SEQ ID NO:1).
US-09-535-008-74

Alignment Scores:
Pred. No.: 1,66e-10 Length: 5477
Score: 192.50 Matches: 82
Percent Similarity: 38.68% Conservative: 53
Best Local Similarity: 23.50% Mismatches: 107
Query Match: 6.26% Indels: 107
DB: Gaps: 16

US-09-687-230a-2 (1-589) x US-09-535-008-74 (1-5477)
Qy      2 G1LysLysHisLysLysHis-----LysSerAspLysHisLeuTyrGlnGluTyrVal 19
Db      4182 GGCTCCCGCCACCGCAAGAGGTGAGTACAGCAGCTCA---CTGACGAGAGCAATGG 4238
Qy      20 GlnLysProLeuLysLeuValLysValGlyGlyAsnGluValThrGluLysSerThr 39
Db      4239 CTCAGACCTGTAAGGCCATC-----4259
Qy      40 GlySerSerLysHisAspSerSerLeuPheGlu---AspLysAsnAspHisAspLysHis 58
Db      4260 -----GAGGAGGCGACGCTGAGAGATTCGAAGAGAGAGCTCCGCGAGAGAAA 4307
Qy      59 LysAspArgLysArgLysLysArgLysGlyGlyLysGlnLysProGlyGlnGluLys 78
Db      4308 TCATACGGAAGGCCAAGCCAGACAGGAGCGCGCTCTTCCACCCGACACCAAGC---4364
Qy      79 GlyArgLysArgArgValLysGluAspLysLysLysArgAspArgAspArgValGlu 98
Db      4365 -----ACCGCAGCGCCGACGAAGAGCAGAGCAAGAAAGCAAGAACCGCGGCGG 4418
Qy      99 AsnGluAlaGluLysAspLeuGlnCysHisAlaProValArgLysAspLysProGlu 118
Db      4419 CCGCGCTGCCGAGAA-----CTCTCCCTTAAC 4445
Qy      119 LysPro-----LeuThrSerSerLeuAlaLysGlnGluLys 130
Db      4446 CCACCCAACTCACCAGAAAGATGAAGAAAGATTGTGATGCGGATCCGATCAAGTAAAGAGC 4505
Qy      131 ValGlnGlnThrProLeuGlnGluValLeuAsnGlnLeuMetArgLysGlnGluArgLys 150

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Db	4602	TTCAAGAAGATAAAGAGCGCATTCGCAACCAAGTACCGGAGCTCAAGCACTTAGAG	4661
Qy	198	Asp ^{Asn} Asp ^{Met} Leu ^{Met} Cys ^{Thr} Asn ^{Ala} Met ^{Ile} Trp ^{Asn} Leu ^{Pro} Glu ^{Thr} Ile ^{Trp}	217
Db	4662	AAGAGCGCATGCTCTGTCGCAGAACGACACTTCAACCTGAGAGGCTCCCTGATC	4721
Qy	218	Tyr ^{Tyr} Ser ^{Ala} Ala ^{Leu} Val ^{Leu} Leu ^{Leu} His ^{Ser} Gly ^{Met} Val ^{Ile} Leu ^{Ser} Glu ^{Ala} Gly ^{Ile}	237
Db	4722	TATTAAGATCTC-----ATCGCTTGACATCGGTCTTC	4754
Qy	238	Gln ^{Ser} Leu ^{Val} Ser ^{Gln} Ser ^{Ile} Asp ^{Pro} Met ^{Ala} Asp ^{Leu} Gln ^{Ile} Thr ^{Arg} Leu ^{Gln} Val ^{Ser}	257
Db	4755	ACCAAGCGGCGGACAAATCAG-----AAGAGAGAT	4787
Qy	258	Asp ^{Gly} Thr ^{Asp} Thr ^{Ser} Gln ^{Ser} Gly ^{Leu} Asp ^{Gly} Gly ^{Cys} Trp ^{Gln} Arg ^{Leu} Glu ^{Ile}	277
Db	4788	GAC-----AGTGAAGCGCAGAGAGACT-----GAGGAGAG	4817
Qy	278	Asp ^{Ser} Gly ^{Asp} Ala ^{Glu} Ala ^{Ile} Ala ^{His} Ala ^{Leu} Ser ^{Pro} Ser ^{Gly} Ser ^{Glu} Asn ^{Leu} Val ^{Ser}	297
Db	4818	GAAAGGGCGGAGAGAAAGCTCCGAATCCGAATTCGCTCGTCAAGTAAGTAAATCAAG	4877
Qy	298	-----Asp ^{Leu} Asp ^{Met} Leu ^{Gln} Asp ^{Leu} Val ^{Ser} Phen ^{Val}	307
Db	4878	CTTGCGCCGGAAGGAGAACGACACAGACCGCGTGAAGGGCGGCGGCGGCGGCGGAGCCGA	4933
Qy	308	-----Ser ^{Asn} Asn ^{Leu} Glu ^{Arg} Glu ^{Gln} Gln ^{Gln} Leu ^{Ile}	318
Db	4938	GGGTCTCCGAGCCAAAGCCGTCGTAGTACGATGACACTGAGAGAGAAACAAGAGAG-----	4994
Qy	319	Asp ^{Arg}	320
Db	4995	GACCGC	5000

```

/ OTHER INFORMATION: Polymorphism of A or G resulting in a silent
/ OTHER INFORMATION: mutation.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (1598)
/ OTHER INFORMATION: Polymorphism of T or C resulting in a silent
/ OTHER INFORMATION: mutation.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (1892)
/ OTHER INFORMATION: Polymorphism of A or G resulting in a silent
/ OTHER INFORMATION: mutation.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (4245)..(4340)
/ OTHER INFORMATION: This is a 96 base insertion compared to SEQ ID
/ OTHER INFORMATION: NO:1.
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (4594)..(4595)
/ OTHER INFORMATION: A deletion of CAG occurs between these bases as
/ OTHER INFORMATION: compared to SEQ ID NO:1 (bases 4499-4501 of SEQ ID
/ OTHER INFORMATION: NO:1).
/
US-09-535-008-68

Alignment Scores:
Pred. No.:      2.5e-10
Score:          191.00
Percent Similarity: 38.15%
Best Local Similarity: 21.53%
Query Match:    6.22%
DB:             4
Gaps:          16
Length:       5564
Matches:      79
Conservative: 61
Mismatch:     113
Indels:       114

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US-09-535-008-68
/ Sequence 68, Application US/09535008
/ Patent No. 6465629
/ GENERAL INFORMATION:
/ APPLICANT: Wong, Alexander K.C.
/ APPLICANT: Tavtigian, Sean V.
/ TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
/ TITLE OF INVENTION: AND OTHER CANCER TYPES
/ FILE REFERENCE: 2318-259
/ CURRENT APPLICATION NUMBER: US/09/535,008
/ CURRENT FILING DATE: 2000-03-23
/ EARLIER APPLICATION NUMBER: U.S. 60/125,806
/ EARLIER FILING DATE: 1999-03-23
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 68
/ LENGTH: 5564
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (75)..(5108)
/ FEATURE:
/ NAME/KEY: conflict
/ LOCATION: (1780)
/ OTHER INFORMATION: GenBank Accession No. 6465629 U29175 shows a C at this
/ OTHER INFORMATION: position (position 1784 in GenBank) rather than
/ OTHER INFORMATION: the G shown here.
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (26)
/ OTHER INFORMATION: Polymorphism of either T or C in this noncoding
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: (1583)

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Db      4182 G G C T C C C G C C A C C C C A A G A G A G C T G A C T A C A G C A C T C A C T G A C G A G A A G C A G T G G C T C 4211
QY      20  G L u b S P r o l e u l y S l e u V a l l e u l y S a l G l y l e u G l u V a l l t h r G l u S e r T h r 39
Db      4242 A A G ----- A A A T T A C A G A A A A G A T T A T C A T T A C A C A G C C A G C 4280
QY      40  ----- G l y S e r S e r 42
Db      4281 A G T G N G C A C G T G G G C T A C A A T T C C A G C G N T G C C T T C A G T T C T G C A C A C G T C A A G 4340
QY      43  G l y h i s a r S e r S e r l e u P h e G l u a s p r l y e h a n s p ----- h i s a r l y h i s l y a s p 60
Db      4341 G C C A T C G G A C G G G C A C G C C T G A G A G A G T C G A A G A G A G G T C C G G A A A G A A T C A T C A 4400
QY      61  A r g l y s a r g l y v l y s a r g l y l y s G l y l u b l y s G l i l e P r o g l y l u G l u l y s G l y A r g 80
Db      4401 C G G A A G C C C A A G C C A G A C A C G A C G C C G G C T C T C A C C C C G A C C A C C A G C ----- 4451
QY      81  L y s a r g a r g a v a l l y s G l u a s p r l y l y s a r g a r g a r a r a r a r a r g a l u a n g l u 100
Db      4452 A C C G C A C C C C C G A C A A G A C A G A C A G A G C A A A G A C A A A G A A G C C C G G C C C C C T 4511
QY      101 A l a g l u l y s a r l e u G l n C y n h i s a l a r o v a l A r g l e u b s r l e u P r o P r o g l u l y e P r o 120
Db      4512 G C C G A G A A ----- C T C T C C C C A A C C A C C C 4538
QY      121 ----- L e u t h s e r S e r l e u a l a l y s G l n G l u l u V a l G l u 132
Db      4539 A A C C T A C C A A G A A G A T G A A A A T T G C A T G C C C G T A C A G T C A A G A G A C A G C A G T 4598
QY      133 G l i n t h r P r o l e u G l n G l u a l e u a n g l i n e u m e t a r g l i n l e u G l n a r g l y a s p P r o 152
Db      4599 G G A C G T C A G C T C A G C A G A G T C T T C A T C A C G T G C C ----- T C G C A A A G A G A G - 4646
QY      153 S e r a l a p h e P h e s e r P h e P r o V a l l t h r a s p h e l l e a l a P r o G l y T y r S e r M e t l l e i l e 172

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Db 4647 -----CTGCCGAGTACTAGACCTCATC 4670
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Qy 193 IleGluLysLeuLysAspAsnPhenylLysLeuMetCysThrAsnAlaMetIleTyrAsnLys 212
Db 4731 CTCAGACACCTAGAGAGAGACGTCATGCTCTGTGCCAGAAACGACAGACCTCAACCTG 4790
Qy 213 ProGluThrIleTyrTyrLysAlaAlaLysLeuLeuHisSerGlyMetLysIleLeu 232
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Db 4824 TTGCAGTCGCTCTTACCAAGGCGGCGGAGAAATTCAG-----4862
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Qy 293 GluAsnLysLysLys-----AspLysAspMetLeuLysAspLysPheLys-----307
Db 4947 AAGTAGAATCAACGCTTGGCGGAGAGAGACAGACAGACCGCTGAAGGCGCGCGG 5006
Qy 308 -----SerAsnGlnLeuGluArg 313
Db 5007 CGGCGCGGAGCGGAGGCTCCGAGCCAGCCGCTCGTAGTACATGACATGACAGTACGAGAG 5066
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RESULT 14
US-08-227-536-1
Sequence 1, Application US/08227536
Patent No. 5658784
GENERAL INFORMATION:
APPLICANT: Eckner, Richard
APPLICANT: Ewen, Mark
APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,536
FILING DATE: 14-APR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: DPCI-308XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 9046 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 1200..8441
US-08-227-536-1

Alignment Scores:
Pred. No.: 6.2e-10 Length: 9046
Score: 190.50 Matches: 130
Percent Similarity: 33.44% Conservative: 83
Best Local Similarity: 20.41% Mismatches: 249
Query Match: 6.20% Indels: 175
Gaps: 26

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Qy 58 HisLysAspArgLysArgLysLysArgLysLysGlyGluLysGlnIleProGlyGlu 77
Db 4116 TCCAGAGAGTGAAGATGAGAGGCCAAATGCAAGTGGATCAACAGAACAGAGATACG 4175
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Qy 98 GluAsnGluAlaGluLysAspLeuGlnCysHisAlaProValArgLeuAspLeuProPro 117
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Qy 134 ThrProLeuGlnGluAlaLeuAsnGlnLeuMetArgGlnLeuGlnArgLysAspProSer 153
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Qy 154 AlaPhe---PheSerPheProValThrAspPheIle-----AlaProGlyTyrSerMet 170
Db 4413 TCCCTTCCCTTGTCTCAACCTGTGAGACCTCAGACTTTAGAAATCCCTGATTTCTTGAT 4472
Qy 171 IleIleLysHisProMetAspPheSerThrMetLysGluLysLysAsnAsnAspTyr 190
Db 4473 ATTGTGAAGAGCCCTCATGATCTTTCTACATTAAGAGAGTAAACATGACATGACATGAT 4532
Qy 191 GlnSerIleGluLysLeuLysAspAsnPhenylLysLeuMetCysThrAsnAlaMetIleTyr 210
Db 4533 CAGGAGCCCTGCGAGATGTCTGATATTTGGCTTATGTTCAATATGCTGTTATAT 4592
Qy 211 AsnLysProGluThrIleTyrTyrLysAlaAlaLysLeuLeuHisSerGlyMetLys 230
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Qy 231 IleLysSerGlnGluArgIleGlnSerLeuLysGlnSerIleAspPheMetAla-----248
Db 4641 GTCTTTGAACAGAA--ATTGACCAAGTACGCAAGCCTTGATGATCTGTCAGAG 4697
Qy 249 -----AspLeuGlnLysThrArgLysGln 256
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Db 4818 GAGATCCAGAGGCGGACGCTTCTTGGGGATGACCTTCCCGCTCAAACTACATA 4877
      ||| ||| ||| |||
Qy 291 SerIleGluAsn---LysLysLysAspLysAspMetLeuGluAspLysPhe---Lys 307
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Db 4878 AATTAAGAACATTTTCCAGAGAAAAATGACACACTGGACTGTAACCTGTTGTTGAA 4937
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Qy 308 SerAsnAsnLeuGluArgGluGlnGluLeu----- 318
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Qy 327 -----GlyLysLeuThrArgArgLeuVal 334
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Qy 335 AsnSerGlnCysGluPheGluArgArgLysProAspGlyThrThrLeuGlyLeuLeu 354
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Qy 415 AspSerThrPheAlaAsnIleSerLysAspAspSerAspLeuIleThr----- 430
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Qy 431 ---SerThrArgLysLysAspSerAspLeuProSerAsp----- 442
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Db 5331 GTTCAAGAGTATGGCTGACTGCTCCACCCCAACAGAGAGATATACATCTTAC 5390
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Qy 443 ---PheSerIleHisGluPheLeuAlaThrCys-----GlnAspLysProThrVal 458
      ||| ||| ||| |||
Db 5391 CTCGATAGTGTCTTCTTCCGCTTAATGCTTGAAGACTGCACTATCATGAAATC 5450
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Qy 459 MetAlaAspSerLeuAspValLeuThrLysGlyLysIleSerArgThrLeuGlnGlu 478
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Db 5451 CTAATTT---GGATATTTAGATATGTCAGAAATTAAGTTACACA----- 5492
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Qy 479 MetGluMetSerLeuProGluAspGluHisThrArgThrLeuAspThrGlyLysGlu 498
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Db 5493 -----ACAAGGCATATTTGGGAGTGTCCCAAGATGAGGGA 5528
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Qy 499 MetGluGlnIleThrGluValIleGluProGlyArg----- 510
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Db 5529 GATGATTAATCTTCATTCCTGCTCTGACCAAGAAATACCAAGCCCAAGGCACTG 5588
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Qy 511 -----LeuAsp----- 512
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Db 5589 CAGGAATGTACAAAAAATGCTGACAGGCTGATCAGAGCGATTTGTCATGACTAC 5648
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Qy 513 -----SerSerThrGlnAspArgLeuIleAlaLeuLysValAlaThrAsn 527
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Db 5649 AAGGATATTTTAAACAAGCTACTGAAATGATTAACAGTGCAGAAAGAAATGCTTAT 5708
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Qy 528 PheGlyValProValIleValIlePheAspSerGluGluIlePheGlnLysLysLeu 547
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Db 5709 TTC-----GAGGATATTTCTGCCCCAATGTTCTG 5738
Qy 548 AspGluThrThrArgLeuLeuArgGluLeuGlnGluAlaGlnAsnGluArg 564
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RESULT 15
PCT-US95-04682-1
: Sequence 1, Application PC/TUS9504682
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: NUCLEIC ACID ENCODING TRANSCRIPTION
: TITLE OF INVENTION: FACTOR P300 AND USES OF P300
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Weingarten, Schurigin, Gagnebin & Hayes
: STREET: Ten Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: US
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04682
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/227,536
: FILING DATE: 14-April-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Holliday C. Heine, Ph.D.
: REGISTRATION NUMBER: 34,346
: REFERENCE/DOCKET NUMBER: DPCI-308X999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-2290
: TELEFAX: (617) 451-0313
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9046 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1200..8441
: PCT-US95-04682-1
:
: Alignment Scores:
: Pred. No.: 6.2e-10 Length: 9046
: Score: 190.50 Matches: 130
: Percent Similarity: 33.44% Conserved: 83
: Best Local Similarity: 20.41% Mismatches: 249
: Query Match: 6.20% Indels: 175
: DB: 5 Gaps: 26
US-09-687-230A-2 (1-589) x PCT-US95-04682-1 (1-9046)
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 Db 4473 ATGTGAAAGAGCCCATGATGATTTTCACTTAAGAGAGAGAGAGACACTGACACTGAT 4532
 QY 191 GlnSerIleGluGluLeuLysAspAsnPheLysLeuMetCysThrAsnAlaMetIleTyr 210
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 QY 231 IleLeuSerGlnGluValGlnIleSerLeuLysGlnSerIleAspPheMetAla----- 248
 Db 4641 GTCCTTGAACAGAA---ATTGACCATGATGCAAAAGCCTTGATCTGTGTGGCAGA 4697
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 QY 257 LysAspGlyThrAspThrSerGlnSerGlyLysAspLysGlyCys----- 271
 Db 4758 CGTGATCCCACTTATTAACGATTAACAGACAGATATCTGTGTGAGAGTGTTCAT 4817
 QY 272 ---TrpGlnArgGluValGluLysSerGlyAspAlaGluAlaHisAlaPheLysSerPro 290
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 Db 4878 AATTAAGAACATTTTCCAAAGAGAAAAATGACACACTGATGATCTGAACTGTTGTGAA 4937
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 QY 375 ThrGlyArgLeuGlnSerGlyValAsnThrLeuGlnGlnLysPheLysGluAspLysArgAsn 394

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 Db 5259 -----CCATACCGAACCAGAACCC----- 5276
 QY 415 AspSerThrPheAlaAsnIleSerLysAspAspSerAspLeuLysTyr----- 430
 Db 5277 -----CTTTGCTTTGAGAAATTTGATGATGTTGACCTGTGCTTTTGGCATCAT 5330
 QY 431 ---SerThrTyrGlyLysAspSerAspLeuProSerAsp----- 442
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 QY 528 PheGlyValProValGluValPheAspSerGluGluAlaGluIlePheGlnLysLysLeu 547
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 QY 548 AspGluThrThrArgLeuLeuArgGluLeuGlnGluAlaGlnAsnGluArg 564
 Db 5739 GAAGAAAGC-----ATTAGGAACCTGAAACAGAGAGAAAGAGAGAGA 5780

Search completed: November 27, 2003, 01:13:18
 Job time : 167 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 27, 2003, 00:55:13 ; Search time 35 Seconds

(without alignments)
3103.917 Million cell updates/sec

Title: US-09-687-230A-2
Perfect score: 3073
Sequence: 1 MGKKHKHKKDKHLYEYVE.....PGNMICLLGPSSEKILINK 589

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*
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3: /cgn2_6/ptodata/2/pubppa/US06_PUB_PUB.pep:*
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5: /cgn2_6/ptodata/2/pubppa/US07_PUB_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppa/US08_PUB_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2972.5	96.7	718	10 US-09-764-864-1579	Sequence 1579, App
2	798.5	26.0	199	10 US-09-764-864-1166	Sequence 1166, App
3	215	7.0	221	9 US-09-925-301-946	Sequence 946, App
4	210.5	6.8	2442	14 US-10-109-886-10	Sequence 10, App
5	205	6.7	1572	12 US-10-116-275-179	Sequence 179, App
6	198	6.4	2441	14 US-10-109-886-8	Sequence 8, App
7	187	6.1	1647	11 US-09-824-574-4	Sequence 4, App
8	183	6.0	580	10 US-09-764-864-1160	Sequence 1160, App
9	181.5	5.9	898	15 US-10-043-487-277	Sequence 277, App
10	179.5	5.8	801	15 US-10-146-473-42	Sequence 42, App
11	167.5	5.5	680	12 US-10-102-143-19	Sequence 19, App
12	164.5	5.4	3051	12 US-10-144-194A-62	Sequence 62, App
13	162.5	5.3	665	11 US-09-820-843A-107	Sequence 107, App
14	160.5	5.2	240	10 US-09-764-864-1168	Sequence 1168, App
15	158	5.1	779	12 US-10-144-194A-86	Sequence 86, App

16	155	5.0	636	12 US-10-032-585-7132	Sequence 7132, App
17	153	5.0	947	15 US-10-293-823-1	Sequence 1, App
18	150	4.9	1938	15 US-10-171-311-164	Sequence 164, App
19	150	4.9	1945	11 US-09-927-597-2	Sequence 2, App
20	150	4.9	1972	12 US-10-341-434-103	Sequence 103, App
21	150	4.9	1972	15 US-10-171-311-162	Sequence 162, App
22	150	4.9	1979	11 US-09-927-597-4	Sequence 4, App
23	149.5	4.9	1087	12 US-10-080-608A-12	Sequence 12, App
24	149.5	4.9	1087	12 US-10-370-688-101	Sequence 101, App
25	149.5	4.9	1312	12 US-10-393-602-148	Sequence 148, App
26	149	4.8	439	12 US-10-354-804-5	Sequence 5, App
27	148.5	4.8	578	15 US-10-137-418A-3	Sequence 3, App
28	148.5	4.8	1390	15 US-10-137-418A-2	Sequence 2, App
29	148.5	4.8	1881	12 US-10-032-585-7666	Sequence 7666, App
30	148	4.8	1104	15 US-10-128-714-3262	Sequence 3262, App
31	148	4.8	1353	15 US-10-128-714-8262	Sequence 8262, App
32	146	4.8	735	12 US-10-144-194A-109	Sequence 109, App
33	146	4.8	784	12 US-10-144-194A-108	Sequence 108, App
34	146	4.8	843	12 US-10-144-194A-84	Sequence 84, App
35	142.5	4.6	128	10 US-09-764-864-1571	Sequence 1571, App
36	142.5	4.6	1170	12 US-10-341-434-95	Sequence 95, App
37	142.5	4.6	1979	15 US-10-205-823-419	Sequence 419, App
38	142	4.6	556	12 US-10-144-678A-1005	Sequence 1005, App
39	142	4.6	556	12 US-10-294-025-1005	Sequence 1005, App
40	142	4.6	556	14 US-10-012-896-1005	Sequence 1005, App
41	141	4.6	505	9 US-09-815-242-11317	Sequence 11317, App
42	141	4.6	505	11 US-09-820-843A-12	Sequence 12, App
43	140	4.6	137	10 US-09-764-864-1581	Sequence 1581, App
44	139.5	4.5	774	12 US-09-949-029-126	Sequence 126, App
45	139	4.5	1703	10 US-09-801-368-340	Sequence 340, App

ALIGNMENTS

RESULT 1
US-09-764-864-1579
Sequence 1579, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1579
LENGTH: 718
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (52)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (99)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1579

Query Match 96.7% Score 2972.5; DB 10; Length 718;
Best Local Similarity 99.1% Pred. No. 2.4e-221; Indels 1; Gaps 1;
Matches 573; Conservative 4;
Db 3 KKKKKKSDGKLVKGVNVEIETSGSGHDSLFEDKNDHKDKRK 62
70 KKKKKKSDGKLVKGVNVEIETSGSGHDSLFEDKNDHKDKRK 129
QY KKKKKKSDGKLVKGVNVEIETSGSGHDSLFEDKNDHKDKRK 122
130 KKKKKKSDGKLVKGVNVEIETSGSGHDSLFEDKNDHKDKRK 189

QY 123 SSLAKOEVEBOTPIQALNOLMROLKRDPSAFSPVTDPIARGYSMITIKHPMDFSTMK 182
DB 190 SSLAKOEVEBOTPIQALNOLMROLKRDPSAFSPVTDPIARGYSMITIKHPMDFSTMK 249
QY 183 EKIKNNDYOSIEELKDNFKLMCTNAMIYNKPEITYYAAKLLHSGMKLLSQRISQILKQ 242
DB 250 EKIKNNDYOSIEELKDNFKLMCTNAMIYNKPEITYYAAKLLHSGMKLLSQRISQILKQ 309
QY 243 SIDPMADLOKTRKQKOGTDSOSGEDGCGWOREDESDGAHAHFKSPSKENKKDKDML 302
DB 310 SIDPMADLOKTRKQKOGTDSOSGEDGCGWOREDESDGAHAHFKSPSKENKKDKDML 369
QY 303 EDKFSNNLEBEREQOLRIYKESGKLTIRLVNSQCEPERKPKDGTTLGLHHPVDPIVG 362
DB 370 EDKFSNNLEBEREQOLRIYKESGKLTIRLVNSQCEPERKPKDGTTLGLHHPVDPIVG 429
QY 363 EPGYCLVRLGNTTGRLOSQVNTLQGFEDKKNKVTPLYLYNGBYSYAPHYSTFANIS 422
DB 430 EPGYCLVRLGNTTGRLOSQVNTLQGFEDKKNKVTPLYLYNGBYSYAPHYSTFANIS 489
QY 423 KDSDDLITYSTYGEDSLPDSFSIHEFLATCODPYRYWADSLDVLTKGHSRTIQEMEMS 482
DB 490 KDSDDLITYSTYGEDSLPDSFSIHEFLATCODPYRYWADSLDVLTKGHSRTIQEMEMS 549
QY 483 LPEDEGHTRLDTEKEMOITEVEPPGRDSSDODRLIALKAVNPGVPEVDFSEAEI 542
DB 550 LPEDEGHTRLDTEKEMOITEVEPPGRDSSDODRLIALKAVNPGVPEVDFSEAEI 608
QY 543 FOKKLDDETRRLRLQEAONEERLSTRPPNMICLLGSP 580
DB 609 FOKKLDDETRRLRLQEAONEERLSTRPPNMICLLGSP 646

RESULT 2

US-09-764-864-1166
; Sequence 1166, Application US/09764864.
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1166
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1166

Query Match 26.0%; Score 798.5; DB 10; Length 199;
Best Local Similarity 41.1%; Pred. No. 6,1e-54;
Matches 176; Conservative 0; Mismatches 1; Indels 251; Gaps 1;

QY 17 EYVEKPLKLVKVGNEVTEISTSSGHDSSLFEDKXNDHDKYKRRKKRKKGEKOIPGE 76
DB 1 EYVEKPLKLVKVGNEVTEISTSSGHDSSLFEDKXNDHDKYKRRKKRKKGEKOIPGE 60
QY 77 EKGKRRRVKEDKKRRDRVNEAEKDLQCHAVRLDLPPEKPLTSSIAQEEVEOTPL 136
DB 61 EKGKRRRVK----- 70
QY 137 QEALNOLMROLKRDPSAFSPVTDPIARGYSMITIKHPMDFSTMKIKNDYOSIEEL 196
DB 71 ----- 70
QY 197 KDNFKLMCTNAMIYNKPEITYYAAKLLHSGMKLLSQRISQILKQSIDPMADLOKTRKQ 256
DB 71 ----- 70
QY 257 KOGTDSOSGEDGCGWOREDESDGAHAHFKSPSKENKKDKDMLDEKFSNNLEBEREQ 316

DB 71 ----- 70
QY 317 QLDRIYKESGKLTIRLVNSQCEPERKPKDGTTLGLHHPVDPIVGPYCLVRLGNTTG 376
DB 71 -----CEFERKPKDGTTLGLHHPVDPIVGPYCLVRLGNTTG 109
QY 377 RLOSQVNTLQGFEDKKNKVTPLYLYNGBYSYAPHYSTFANISKDSDDLITYSTYGED 436
DB 110 RLOSQVNTLQGFEDKKNKVTPLYLYNGBYSYAPHYSTFANISKDSDDLITYSTYGED 169
QY 437 SDLPDSFS 444
DB 170 SDLPDSFS 177

RESULT 3

US-09-925-301-946
; Sequence 946, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; Prior application number: PCT/US00/05882
; Prior filing date: 2000-03-08
; Prior application number: PCT/US00/05882
; Prior filing date: 2000-03-08
; Prior application number: 60/124,270
; Prior filing date: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 946
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-946

Query Match 7.0%; Score 215; DB 9; Length 221;
Best Local Similarity 28.8%; Pred. No. 1e-08;
Matches 60; Conservative 48; Mismatches 76; Indels 24; Gaps 8;

QY 371 LGMTTGRLOSQVNTLQGFEDKKNKVTPLYLYNGBYSYAPHYSTFANISKDSDDLITY 430
DB 8 LSSLSKLLPGFTTL-GFKDERRNKVT---FLS-SATTALSMONNSVFGDLKSDMEMLTY 62
QY 431 STYGEDSDLPDSFSIHEFLATCODPYRYWADSLDVLTKGHSRTIQEME-----MSLP 484
DB 63 SAVGDETVGCALSLQGFVNDAGSYKVVDDLDLDTGGHSHSLFOLKORRVNPKKPP 122
QY 485 EDEGHTRTL-DTGKEMOITEVEPPGRDSSDODRLIALKAVNPGVPEVDFSEBAEIP 543
DB 123 DEAKVGTTLDSSSVLEFRSMK-----SYRPSVDISMLSLGVKKELDDDDHL- 174
QY 544 QKKLDDETRRLRLQEAONE--RLSTRP 569
DB 175 --NLDETTKLLQDLHBAQADAAALGXRP 200

RESULT 4

US-10-109-886-10
; Sequence 10, Application US/10109886
; Publication No. US20020119499A1
; GENERAL INFORMATION:
; APPLICANT: TANABE SEIYAKU CO. LTD.
; APPLICANT: TANIGUCHI, Tomoyasu
; APPLICANT: MIZUKAMI, Junko
; TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPAR

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: FILE REFERENCE: TANIGUCHI-6
: CURRENT APPLICATION NUMBER: US/10/109,886
: CURRENT FILING DATE: 2002-04-01
: PRIOR APPLICATION NUMBER: 09/514,247
: PRIOR FILING DATE: 2000-02-28
: PRIOR APPLICATION NUMBER: PCT/JP98/03734
: PRIOR FILING DATE: 1998-08-24
: PRIOR APPLICATION NUMBER: JP231084/1997
: PRIOR FILING DATE: 1997-08-27
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 10
: LENGTH: 2442
: TYPE: PRT
: ORGANISM: human
: US-10-109-886-10

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Query Match	6.8%;	Score 210.5;	DB 14;	Length 2442;
Best Local Similarity	21.2%;	Pred. No. 6.9e-07;		
Matches 143;	Conservative 80;	Mismatches 213;	Indels 239;	Gaps 32;

QY	36	ELSTGSSSHDSSSLPFEDKND---	HDHGKROKXKRRKKKGKQJ	PGEKGGKRRRVVED	88		
Db	982	ETNSQOCPDPVLYEMKTETOEDTEPD	-----	PBSKSGPRSRMEWEDLQG	1028		
QY	89	--KKRDRDRVENEAENDLOCHAPRYLD	LPPEKPLTSLAKQEEVEOT	-----	134		
Db	1029	ASQVKEEDIDAEQSE	-----	PHEVD--EKKPEVKVEVEEBSSSSNGTASOSTSPSQ	10779		
QY	135	-----	PLQBALNQMLROLQKQDSAF--	FSPFVTDFT--	APGYSMIHKPMDFSTMK	182	
Db	1080	PRKFIKPEEELRQALMPLTLEALYRDP	PESTLPPRGVDPQLGIPDYIVK	PNMPLSTIK	1139		
QY	183	EKIKKNDVQSIBELKDNFKLMCTN	AMITNKETIYYKAAKULHSGMKILS	QERIQSLQK	242		
Db	1140	RKLDGTGOYQEPWQYVDVWLMFN	NMAMLNKRTISRYYKCSXL	-----	AEVFOE--IDPFWQ	1194	
QY	243	SIDPMA	-----	DLQTRKQXQDGTDSQSEBDGC	-----	WORERERDSDA	282
Db	1195	SLGICCGRKRYFSPOTLCYCQKOLCT	IPRDAAYISQNRHYHCEKCFTEIO	GENVTIJD	1253		
QY	283	EAAHFKSPSKENKKKDKMLLEDKFS	NNLE	-----	REOEOL	318	
Db	1254	-----	DPSQQTITSKDQFEKK--	KNDTLDPEPFVDCKE	CGRKXHQICLVH	YDIWPSGF	1306
QY	319	--DRIVKESG	-----	GKTRRLVNSQCEFERRKDPD	GTTLGLHPVDIV	361	
Db	1307	VCDNCLAKTKGPRKRNKFSAKRLQ	TRRLGNHLEDRVNFRLRON	-----	HP	1352	
QY	362	GEPEYCLVRLGMTGRLOS	GVNTLQGFEDKRNKVTPL	--	YANYGPRYSIAHP--	YDST	417
Db	1353	-EAGEVFPRVVAAS	-----	DTIVEKPKMKSRFVDSG	SMSSFPRTVAL	1396	
QY	418	FANISKDSDLIY	-----	STYGEDSLPSD	-----	FSIHEFLATC--QDYPYVAD	461
Db	1397	FAFEIDGVDCFGMHVQAYGSDCP	PPNTRRVYISYDLSIHFFPR	PLRATVAVHEIIG	1456		
QY	462	SILDVLTKG--	GHSRTLQEMEMSLPEDEG	-----	HTRTLDTGKEMEQITEVEPGRJD	512	
Db	1457	YLEVYKKLGYVTGHI	-----	WACPRSEGDYIFHC	PPD--QKIPPKRLQE	1501	
QY	513	-----	SSTODRLIALKAVTNFGV	VEVDSSEAEIFQKJLDE	549		
Db	1502	WYKMLDKAFARIIDHYKDIF	KOATEDRLTSAKELPYF	-----	EGDFWPNVLEE	1551	
QY	550	TTRLRLRELOEQANER	564				
Db	1552	S--IKELQEEER	1563				

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; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elian Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 179
; LENGTH: 1572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-179

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Query Match	6.7%	Score 205;	DB 12;	Length 1572;
Best Local Similarity	23.5%;	Pred. No. 9.8e-07;		
Matches 82;	Conservative 56;	Mismatches 99;	Indels 112;	Gaps 14;

[illegible]

RESULT 6
US-10-109-886-8
Sequence 8, Application US/10109886
Publication No. US20020119499A1
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUTANI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND
FILE REFERENCE: TANIGUCHI-6
CURRENT APPLICATION NUMBER: US/10/109,886
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 09/514,247
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/J98/03734
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 2441

TYPE: PRT
ORGANISM: mouse
US-10-109-886-8

Query Match 6.4%; Score 198; DB 14; Length 2441;
Best Local Similarity 19.9%; Pred. No. 6.4e-06;
Matches 139; Conservative 93; Mismatches 219; Indels 248; Gaps 29;

QY 32 NEVTELTSSGSHSSLPEDKNDHDKKDRKKRKKKGGKQIPDEEGRKRRKED--- 88
DB 971 NRPVPTSTVSAETSS--QQPGPVMLEMTKEVQTDABEPFESKGEPRSEMEEDLQ 1028
QY 89 ---KKKDRDRVENEAEKDLOCHAPVRLDLPPEKPLTSSLAKEVEQT----- 134
DB 1029 GSGVKEETOTTEKSEF-----MEVEKKEPEVKEVEKEEENSSNDTASQSTSPS 1079
QY 135 -----PLOBALNQLMKROLQKPSAF--FSFVPTDFI--APGSMIIKHPMDFSTM 181
DB 1080 QPRKKIPEPELRQALPTEALYRQDPESLPFRQPVDPOLGIPDYFDIVKPMDSLTI 1139
QY 182 KKKIKNNDYQSIIEBKONFKLMCTNAMIYKPEITYYKAAKLIHSGMKLISQRIQSLK 241
DB 1140 KKKLDTGQYQEPWQYVDVRLMENNANWLYNRKTSRYVKFCSKL---AEVFEDE-IDPVM 1194
QY 242 QSIDFMADLQKTRKQKQDGT-----SOSGEDGCGW---QERE 277
DB 1195 QSLGCGG---KRYERSPTLCCYKQOLCTIPDAAYISQNRHYHCGKCFTEIQGENV 1250
QY 278 DSGDAEHAFAKSPSKENKKDKMLIEDKPKSNMLE-----REQEOL----- 318
DB 1251 TLGD-----DPSQPTTISKQDFEKK-KNDTLDPEPFVDCKEGKRMHQLCVLHYDII 1302
QY 319 -----DRIVEEG-----GKTLRLVNSOCEPERKRPDGTTLGLLHP 356
DB 1303 WPSGFVCDNCLKTKGRPRKKNKPSAKRLQTTRLGNHLEDRVYKFLRRQN-----HP 1353
QY 357 VDPVIGEPGYCLVRLGWTGTRLSGVNTLQCFKEDKKNKVPVL---YLVNGPYSSYAPH 413
DB 1354 -----EAGEVFAVRVASS-----DKTVEKFKPKSKSFVDSGESESEFPY 1392
QY 414 -----YDSTFANISKDSOLI-----YSTGEGSDLPSPDSIHEPLAT 451
DB 1393 RTKALFAFEEDVDVCFPGMHVQDTALIAHQIQCVCYISYLD-----SIHFRPR 1444
QY 452 C-----QDYPYMADSLVDLTGCG-----HSTTLQEME 480
DB 1445 CLRTAVYHEILIGYLEVYKLVVYTAHIMACRPSBGDYIFCHPRDQKIPKPRQLQEWY 1504
QY 481 MSIPDEGHTRLDTGKEMQITEVEBPGRLSSTODRLALKAVTFNGVVEVDFDEEA 540
DB 1505 KKLMDKFAFRIINDYDI-----FKQANERLISAKELPYF-----EG 1543
QY 541 EIFOKKLDFTTRLLRELQEAQNER-----LSTRPPGN 572
DB 1544 DFWPNVLEES---IKELQEEERKKESTAASETPGS 1579

RESULT 7
US-09-824-574-4
Sequence 4, Application US/09824574
Publication No. US20030077800A1
GENERAL INFORMATION:
APPLICANT: Rouleau, Natalie
APPLICANT: Moilanen, Anu-Maarit
APPLICANT: Palvimo, Jorma J.
TITLE OF INVENTION: Arp4 Gene and Protein
FILE REFERENCE: 2630-109
CURRENT APPLICATION NUMBER: US/09/824,574
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4

LENGTH: 1647
TYPE: PRT
ORGANISM: Homo sapiens
US-09-824-574-4

Query Match 6.1%; Score 187; DB 11; Length 1647;
Best Local Similarity 23.1%; Pred. No. 2.6e-05;
Matches 77; Conservative 53; Mismatches 118; Indels 86; Gaps 14;

QY 7 KKSXDKLYEYVEKPKLVKVGNEVTELTSSGSHSSLPEDKNDHDKKDRKKR 66
DB 1372 RHRKEVDYSDLTETKQWLKAIIEGTLEIEI-----BEVROKSSRRKRD 1416
QY 67 KKEGKQIPGEKRRKRRRVEDKKKDRDRVENEAEKDLOCHAPVRLDLPPEKPLTSSL 125
DB 1417 SDAGSSTPTTS---TMSRDQDESKQKQKGRPAEK-----LSPNPNLTXX-- 1460
QY 126 AKQEEVEQTPLOBALNQLMKROLQKPSAFSPVPTDFIAPGYSMIIKHPMDFSTM 185
DB 1461 -KKKKIVDAVIKYKSSSGRQLS---EVFIQLPSRREL-PEYVELIRKVPDFKIKERI 1514
QY 186 KANDYQSIIEBKONFKLMCTNAMIYKPEITYYKAAKLIHSGMKLISQRIQSLK 245
DB 1515 RNHKYSLNDLEKDVMLCQNAQTFNLESLIYEDS-----IVLQSVFTSVROKIE 1565
QY 246 FMADLQKTRKQKQDGTSSGEGCGQREEDSGAFAKSPSKENKK---DKDMLE 303
DB 1566 -----KEDD-----SEGEES-----EEEGEESGESRSVYKIKLGRKEKAQ 1606
QY 304 DKFK-----SNMLEREQQLDR 320
DB 1607 DRUKGRRRPSRGRAPKPVVSDDSSEDEGE-DR 1639

RESULT 8
US-09-764-864-1160
Sequence 1160, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1160
LENGTH: 580
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-864-1160

Query Match 6.0%; Score 183; DB 10; Length 580;
Best Local Similarity 19.8%; Pred. No. 1.2e-05;
Matches 102; Conservative 73; Mismatches 155; Indels 184; Gaps 19;

QY 9 KSDKHLYEYVEKPKLVKVGNEVTELTSSGSHSSLPEDKNDHDKKDRKKR 68
DB 53 RNDKYAGEEGMIDMKLMFNARHYNBE-----GSQYVYDA--HILEKLKEKREKL 102
QY 69 GEKQIIGEEKGRKRRVKEKKKDRDRVENEAEKDLOCHAPVRLDLPPEKPLTSSLAKQ 128
DB 103 G--PLPDDDD-----MASPKLTLNR-----KSGISPK 127
QY 129 EEVEQTPLOBALNQLMKROLQ-----RKPSAFSPVPTDFIAPGYSMIIKHPMDFSTM 181
DB 128 KSKYTMFMQKLVNEVAVKAYITDKGRRLSAFLPLPSSEL--PDYIYLTKKPMDEKI 186
QY 182 KKKIKNNDYQSIIEBKONFKLMCTNAMIYKPEITYYKAA-----KKLHLS----- 227
DB 187 RSHMANKQDDIDISVDEDFVMFNNACTYNEPSLTYKDALVHLKVLLETRRDLGDEDS 246

QY 228 ---GMKLSOERIQSLOSI----- 244
DB 247 HVENVTLLIQELLHNFVSVSHQDDGRCYSDSLAEIPAVDNFPNPKPLFTDITRKXV 306
QY 245 -----DPMADLOKTRKQKQDTDSOGSDGCGMOR-----ERESGD----- 281
DB 307 ENNRVRLDFOQHMEFEVLERARRMNTD-SEIYEADVELQOFPKIRDLCKNGELLIS 365
QY 282 -----AEAHAFKSPSKENKKK-DKMDLEDKFSNNLEREOOLDRIYKESGKLTIRLVN 335
DB 366 PALSYTTKHLANDVEKERKELKREIREDYDKREBERKEKESDSSGAAGLSGHRHTYS 425
QY 336 SOCFERRRRKPDGTTTGLAPVDPVIGEPG-----YCLVRLGMTTGRLOSQVNTLQG 387
DB 426 QDCSFKN-----SMYHVGDVYVYEPABANLQPHIVICIERLMEDS-----AGEKMLYG 472
QY 388 -----FKEDKRNKVTVPV 399
DB 473 CWFYRNETFHLATRKFLKEKEVFKSDYNNKV-PV 505

RESULT 9

US-10-043-487-277
; Sequence 277, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptid
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 277
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Shigella flexneri
US-10-043-487-277

Query Match 5.9%; Score 181.5; DB 15; Length 898;
Best Local Similarity 21.0%; Pred. No. 2.9e-05;
Matches 118; Conservative 81; Mismatches 195; Indels 167; Gaps 21;

QY 6 KKHSDKHLVEEYVEKPLKLVKVGNEVETELSTGSSGHSLSLFEEDKNDHDKHKKRKK 65
DB 380 KKRVTGTTCVCDYLNRPKHSIHRRRTDPMVTLSSILESTINDMRDLPNTYPTFTPVNAKY 439
QY 66 RKKGGEQIQEEEGKRRKRYKEDKKR--DRDR-----VENAEKDLOCHAPVR-- 112
DB 440 VVDYKTI--TRPMLOTLRENVKRLKLPSEEFREHLELIYKNSATYNGPGHSILQIS 496
QY 113 ---LDLPREKPLTSLAKOEVEQTPLOEALNOLMQLOKDPSAF----- 155
DB 497 QSMULDCEK-----LKEKEDLARLEKAINPL--LDDDDVAASFLINDIVTQKMA 547
QY 156 -----FSPVPTDFIAPGYSMIIKHPMDFSTMKETIKNDYOSIEELKDNFKLMCTNAMI 209
DB 548 VPDSPWFHHPVNNKKFVPDYKVIIVNPMDELITIRKNSIKHKYQSRSEFLDDVNLILANSYK 607
QY 210 YNKPEITTYKAAKLIHSGMKILISQ--ERISQSLK-----QSIDPMADLO 251
DB 608 YNGPESQYTKAQEIIVNVCQTLTEVDENHLOLEKQICTAKAALAEAELESIDPMTPGP 667
QY 252 KTRKQKDGTDTSOS---GEDGCGMOREREDS--GDAEAHAFKSPSKENKKKXD----- 300
DB 668 YTFQPPDLVDINTSLMSRDSYVFQDESNNVLDIDISAPPEKQVTOBEGDGDGLADEEB 727
QY 301 -----MLDEKFSNNLEREOOLDRIYKESGKLTIRLVNQCCEFERRRKPDGTTT 350

DB 728 GTVQOPQASVLYEDLMS---EGEDEDEADGSDDEBDN-----PFSAIQLSESGSDSDVG 779
QY 351 LGLHNVDPPIVGBPGVCLVRLGTTGRLOSQVNTLQFKEDKRNKXTVPVY----- 401
DB 780 SGGIRKQPRM-----LOE--NT-----RDMENESMWSYEGDGBASH 817
QY 402 -----LNYGYSYVAPH---YDSTPANI----- 421
DB 818 GLEDSNISYSGYSEPPPKSNTQDTSFSISIGYEVSRSEBDEBEDEBQSRGSPVLSQVHLSE 877
QY 422 SKDSDPLITYTGEDSDLPD 442
DB 878 DEEDSEDFHSIAG-DEDLDD 897

RESULT 10

US-10-146-473-42
; Sequence 42, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: U00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 801
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-42

Query Match 5.8%; Score 179.5; DB 15; Length 801;
Best Local Similarity 27.2%; Pred. No. 3.5e-05;
Matches 67; Conservative 36; Mismatches 90; Indels 53; Gaps 10;

QY 110 PVRLDPEPKPLTSLAKOEVEQTPLOAL---NOLMQLOKDPSAF--FSPVPTDF 163
DB 323 PIK---PPRKDLPSDQSQHSSKKGKLSQLKHCNGLKELLSKKAAYAMPFYKCV-DA 378
QY 164 IAPG--YSMIIKHPMDFSTMKETIKNDYOSIEELKDNFKLMCTNAMIYNKPETIYYKA 220
DB 379 SALGLHDYDITKHPMDSLTVKRNENRDRDAQEPADVRLMFSQYKYNPDHDVAM 438
QY 221 AKKL-----LHSGMKILSOERIQSLOSIQSIDPMADLOKTRKQKQDTDSOS 265
DB 439 ARKLDQVFERYAKWDEPLEPGPLVSTAMPGL-----AKSSSESSSES 485
QY 266 GEDGCGMOREREDSGDAEAHAFKSPSKENKKKDKMDLEKFSNNLEREOOLDRIYKES 325
DB 486 SSSSESSSEEBDEBDEE-----EBESSSDSEEB--RAHRLAEQOL-RAVHEQ 533
QY 326 GSKLTR 331
DB 534 LAALSO 539

RESULT 11

US-10-102-143-19
; Sequence 19, Application US/10102143
; Publication No. US20030185851A1
; GENERAL INFORMATION:
; APPLICANT: Soldati, Dominique
; APPLICANT: Meisner, Markus
; TITLE OF INVENTION: TET transactivator system

```
FILE REFERENCE: 04630/016001
CURRENT APPLICATION NUMBER: US/10/102.143
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 680
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-10-102-143-19

Query Match
Best Local Similarity 5.5%; Score 167.5; DB 12; Length 680;
Pred. No. 0.00024;
Matches 36; Conservative 24; Mismatches 42; Indels 1; Gaps 1;

123 SSLAKOE-VEQPLQELNQLMROLOKDPASAFSPVTDPLAGYSMTIKHPMDFSTM 181
Db 564 AGRAKEGKLRASLSKAOIALSLTEKSSSWFRRPVSEAPDYEVVRRRIDSLTM 623

Qy 182 KERIKNNDYOSIELKDNFKLMCTNAMIYKPEIYYKAATL 224
Db 624 KKNRNGDYRTKEAFQEDLLMFQNCRVNSPTIYYKVADEL 666

RESULT 12
US-10-144-194A-62
Sequence 62, Application US/10144194A
Publication No. US20030215809A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144.194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn version 3.0
SEQ ID NO 62
LENGTH: 3051
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-194A-62

Query Match
Best Local Similarity 5.4%; Score 164.5; DB 12; Length 3051;
Pred. No. 0.0035;
Matches 126; Conservative 102; Mismatches 249; Indels 153; Gaps 24;

Qy 16 EBYVEKPLKVLKVGNEVTELTSGSGHDSLFEDKNDHDKHKRRKKKGEKQIPG 75
Db 278 EEFSDLC-----PVEIKYTYEHNHLLILNKDVQESSEQKKSTDKGEKQIPG 328

Qy 76 EKKGRKRRRYKE-----DKKKRDRRVENE--AEKDLQCHAPVRLDLPPEKPLTSS 124
Db 329 NEKERKKEKEKEKEKEKEDPHKSEDTQKVKDEQAKKEKEV-----SLKLPSEK---N 379

Qy 125 LAKOEVEQPLQELNQLMROLOKDPASAFSPVTDPLAGYSMTI--KHPMDFSTM 181
Db 380 SNKAKTYEGT-----KED-----FSLIDSDVDGJLDLIVSSVHTSDLSSEF 419

Qy 182 KE-----KIKNNDYOSIELKDNFKLMCTNAMIYKPEIYY-----YK 219
Db 420 EEDTEEBVYVTSDSMEBEITSDDE--EKNKQNTKTQTSSESGKTSVHNAVYHREYL 476

Qy 220 AAKLLHSGMKILSGKILSGKILSGKILSGKILSGKILSGKILSGKILSGKILSGK 270
Db 477 YSKYSSDSDELTYEQRRQSLAKEKEKELRLRQIN-REKLEEKQKQAKKSKSKTKGQ 535

Qy 271 CWQREEDSGG---DAEAAAFKSPSKENKQDKOM-LEDKFKSNLLEQEQDLRIYKES 325
Db 536 RSVVDLESSSTKSLKPEPKARITKEVLRKERVLEKKVVALSKKKKQDSRVNEENS 595
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Qy 326 GGLTRRLVNSQCEFERRRKPDGTTTGLLHPVDPIVEBQCYCLVRLGTTGRLQSGVNTL 385
Db 596 DSKETLK-TSEHC--EKELISSSEKELKHVH---AKSEPSKPARRLSESLHVDENKNES 648

Qy 386 QCFKEDKRNKVTPLVLYNAGYSSVAPHYDSTFANISKQDSLDLYSTYGEDSLPDPFSI 445
Db 649 KIEREHRRTSTFVI-----MEGVQESTDTRDVRQOVERSSI----- 665

Qy 446 HEFLATCODYPYVMADSLDLVLTGKHSRTLQEMEMSLPEDEGHTRTLDTGKEMEQITTEV 505
Db 686 -----CTEPPQOKSKTL-----KNEGLKKDSETHLKSLLKKEVYSSK 725

Qy 506 EPPGRDSSDQDLRLAK-----AVTNFQVPEVDFDSEBAE1FOKKLDETTLLBELQ 559
Db 726 EKPEREKTPESDKL-SVKHKYKGDCHMKTGDETELHSSSEKGLKVEENIQOSQOTKLSSD 784

Qy 560 AONERLSTRPPGMICLLG-----PSEKCI 585
Db 785 DKTERKSKHNRERKLSVLGDKGPVSEYII 814

RESULT 13
US-09-820-843A-107
Sequence 107, Application US/09820843A
Publication No. US2003003963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820.843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 107
LENGTH: 665
TYPE: PRT
ORGANISM: Plasmodium falciparum
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: hypothetical protein
NAME/KEY: misc feature
OTHER INFORMATION: g1|3845248
US-09-820-843A-107

Query Match
Best Local Similarity 5.3%; Score 162.5; DB 11; Length 665;
Pred. No. 0.00056;
Matches 67; Conservative 57; Mismatches 107; Indels 97; Gaps 12;

Qy 6 KKHSDGHLVEEYVEKPLKVLKVGNEVTELTSGSGHDSLFEDKNDHDKHKRRKK 65
Db 295 KKEIDKTHLBE-----ENEIIEKE-----FSDKKQKQKNDTKKEK 331

Qy 66 RKKEGKO---IPGE- KGRKRRRYKEDKKRDRRVENAEKDLQCHAPVRLDLPPEK 120
Db 332 SKDTEKESKQDIEKESKQDIEKESKQDIEKESKQDIEKESKQDIEKESKQDIEKESK 390

Qy 121 LTSSLAQF-----EVEQTPLOELNQLMROLOKDPASAFSPVTDPLAGYSMTIIGHPM 176
Db 391 KDTAKEKEKQDIEKESKQDIEKESKQDIEKESKQDIEKESKQDIEKESKQDIEKESK 427

Qy 177 DFTMKERIKNNDYOSIELKDNFKLMCTNAMIYKPEIYYKAKKLLHSGMKILSGK 236
Db 428 -----EK-KKNDKODIHDND-----ENDM-----EE 449

Qy 237 IOSLKOSIDPMADLOKTRKQKQDGTDSQSGEDGCWQREBDSGDAEAAAFKSPSKENK 296
Db 450 IEBNDBEDDEDEDMENKKKKKKGNNGNENG--SENGNENGNENGNENGNENGNES 507

Qy 297 KDKMLEDKFKSNLLEQEQDLRIYKE 324
Db 508 NENENENGNENGNENGNENGNENGNENGNENGNENGNENGNENGNENGNENGNENGNEN 534
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OM protein - protein search, using sw model

Run on: November 27, 2003, 00:37:26 ; Search time 22 Seconds

(without alignments)
1132.777 Million cell updates/sec

Title: US-09-687-230a-2

Perfect score: 3073
Sequence: 1 MGKKHKKKSKDKHLVEEYVE.....FGNNICLLGPSSEKCIILNK 589

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4210858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued Patents AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3073	100.0	589	3	US-08-942-008-2
2	685	22.3	159	4	US-08-747-562-30
3	210.5	6.8	2442	4	US-09-514-247A-10
4	198	6.4	2441	1	US-08-194-468-2
5	198	6.4	2441	3	US-08-961-739-2
6	198	6.4	2441	4	US-09-514-247A-8
7	192.5	6.2	1649	4	US-09-535-008-75
8	191	6.2	1650	4	US-09-535-008-71
9	191	6.2	1678	4	US-09-535-008-69
10	190.5	6.2	2414	1	US-08-227-536-2
11	190.5	6.2	2414	5	PCT-US93-04682-2
12	189.5	6.1	1646	4	US-09-535-008-67
13	188.5	6.1	1646	4	US-09-535-008-65
14	188.5	6.1	1681	4	US-09-535-008-77
15	187	6.1	1647	4	US-09-535-008-2
16	187	6.1	1682	4	US-09-535-008-73
17	181.5	5.9	1872	1	US-08-188-582-14
18	181.5	5.9	1872	1	US-08-646-715-14
19	181.5	5.9	1893	1	US-08-188-582-11
20	181.5	5.9	1893	1	US-08-646-715-11
21	153	5.0	947	4	US-09-418-780A-1
22	150.5	4.9	1312	2	US-08-687-080-51
23	149.5	4.9	1087	4	US-09-914-259-12
24	149.5	4.9	1312	2	US-08-592-126-148
25	149.5	4.9	1312	4	US-09-168-595-148
26	147.5	4.8	1588	5	PCT-US93-07261-11
27	147.5	4.8	1663	5	PCT-US93-07261-16

28	146.5	4.8	2662	4	US-09-595-684B-31	Sequence 31, Appl
29	144	4.7	800	4	US-09-555-790A-2	Sequence 2, Appl
30	144	4.7	1866	4	US-08-938-105-3	Sequence 3, Appl
31	142	4.6	1898	1	US-08-056-200-94	Sequence 94, Appl
32	142	4.6	1898	2	US-08-800-644-94	Sequence 94, Appl
33	142	4.6	3248	4	US-08-353-700-1	Sequence 1, Appl
34	142	4.6	3248	5	PCT-US95-16216-1	Sequence 1, Appl
35	141.5	4.6	2482	1	US-08-328-254-6	Sequence 6, Appl
36	140	4.6	1939	4	US-09-310-187A-1	Sequence 1, Appl
37	138.5	4.5	765	2	US-08-663-112-2	Sequence 2, Appl
38	138.5	4.5	885	4	US-09-914-259-10	Sequence 10, Appl
39	138.5	4.5	1196	4	US-09-107-532A-3944	Sequence 3944, Ap
40	135	4.4	8991	4	US-08-714-741-32	Sequence 32, Appl
41	133.5	4.3	1161	4	US-09-337-536-2	Sequence 2, Appl
42	133	4.3	967	4	US-09-914-259-21	Sequence 21, Appl
43	133	4.3	3878	4	US-09-914-259-11	Sequence 11, Appl
44	132.5	4.3	1388	2	US-08-685-576-4	Sequence 4, Appl
45	130.5	4.2	1404	4	US-08-801-308-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-942-008-2
Sequence 2, Application US/08942008
Patent No. 6133419
GENERAL INFORMATION:
APPLICANT: Baselmann, Sylvia
TITLE OF INVENTION: Nucleotide Sequences that Encode
TITLE OF INVENTION: Phosphatidylinositol-3' Kinase Associated Proteins and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: CA
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,008
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gioceta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX1027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 262-8710
TELEFAX: (510) 222-9758
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-942-008-2
Query Match 100.0%; Score 3073; DB 3; Length 589;
Best Local Similarity 100.0%; Pred. No. 4,8e-262;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MGKKHKKKSKDKHLVEEYVEPLKLVKVGNGEYTELSTSSGGHDSLFEDKNDHDKKD 60
Db 1 MGKKHKKKSKDKHLVEEYVEPLKLVKVGNGEYTELSTSSGGHDSLFEDKNDHDKKD 60
Cy 61 RKRKRKKKKKQIPGEKKGKRRRVKEDKKKRDVRVNEAKNDLQCHAPVRLDLPEKRP 120

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Db 61 RRRKKKKKKQIIGEEKGRARRVKEKKKKRDRDVENAEKQLQCHAPRDLDPREKP 120
Qy 121 LTTSLAKOEVEQPTPLQALNQLMRQORQPSAFSPPTDTFAPGYSMITIKPMDBST 180
Db 121 LTTSLAKOEVEQPTPLQALNQLMRQORQPSAFSPFPVDTFAPGYSMITIKPMDBST 180
Qy 181 MKKIKKNNDDYOSIEELKDNFKLMCTNMTYKPEITTYKAAKLLHSGMKLLSGERTSL 240
Db 181 MKKIKKNNDDYOSIEELKDNFKLMCTNMTYKPEITTYKAAKLLHSGMKLLSGERTSL 240
Qy 241 KQSIDFMADLOKTRKQKQDGTDTSSQSGEDGCMQEREDSGDAEAHAFSPSEKMKKDXD 300
Db 241 KQSIDFMADLOKTRKQKQDGTDTSSQSGEDGCMQEREDSGDAEAHAFSPSEKMKKDXD 300
Qy 301 MLEDFKSNLNEREOQLDRIVKESGKLTRLVNSQCEFFRRKPDGTTTGLLHPVDPI 360
Db 301 MLEDFKSNLNEREOQLDRIVKESGKLTRLVNSQCEFFRRKPDGTTTGLLHPVDPI 360
Qy 361 VGEFGYCLVRLGTTTGRLOSQVNTLQGFKEKRNKVPVLYLNGPSSVAPHYDSTFAN 420
Db 361 VGEFGYCLVRLGTTTGRLOSQVNTLQGFKEKRNKVPVLYLNGPSSVAPHYDSTFAN 420
Qy 421 ISKDSDLIYSTYGEDSDLPSPDFSIHEFLATCQDYPYVADSLDLVLTGSHSRTLQEME 480
Db 421 ISKDSDLIYSTYGEDSDLPSPDFSIHEFLATCQDYPYVADSLDLVLTGSHSRTLQEME 480
Qy 481 MSLEPDEGHTRTLDTGKMEQITEVEPPRLDSDTODRLALKAVTNGVPEVDFSEEA 540
Db 481 MSLEPDEGHTRTLDTGKMEQITEVEPPRLDSDTODRLALKAVTNGVPEVDFSEEA 540
Qy 541 EIFQKKIDETTRLRLRELOEAGNERLSTRPPGNMCLLGPSSSEKCLLNK 589
Db 541 EIFQKKIDETTRLRLRELOEAGNERLSTRPPGNMCLLGPSSSEKCLLNK 589

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RESULT 2

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US-08-747-562-30
; Sequence 30, Application US/08747562
; Patent No. 6579697
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BOLDIN, Mark
; APPLICANT: METT, Igor
; APPLICANT: VAREFOLOREV, Eugene
; TITLE OF INVENTION: MODULATOR OF TNF/NGF SUPERFAMILY RECEPTORS
; TITLE OF INVENTION: AND SOLUBLE OLIGOMERIC TNF/NGF SUPERFAMILY RECEPTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,562
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05854
; FILING DATE: 11-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109,632
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 111,125
; FILING DATE: 02-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.

```

```

; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-15A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-747-562-30

```

Query Match 22.3%; Score 685; DB 4; Length 159;

Best Local Similarity 91.3%; Pred. No. 1.2e-52; Indels 2; Gaps 2;

Matches 136; Conservative 3; Mismatches 8; Indels 2; Gaps 2;

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Qy 274 REREDSGD-AEAAHAFKSPSEKNNKKKKMDLEDFKSNLNEREOQLDRIVKESGKLTTR 332
Db 5 RERERTLEVAEAAHAFKSPSEKNNKKKKMDLEDFKSNLNEREOQLDRIVKESGKLTTR 64
Qy 333 LVNSQCEFFERRKPDGTTTGLLHPVDPIVGEFGYCLVRLGTTTGRLOSQVNTLQGFKEBK 392
Db 65 LVNSQCEFFERRKPDGTTTGLLHPVDPIVGEFGYCLVRLGTTTGRLOSQVNTLQGFKEBK 124
Qy 393 RNKVTPLYLNL-YGPSSVAPHYDSTFAN 420
Db 125 RNKVTPLYLNL-YGPSSVAPHYDSTFAN 153

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RESULT 3

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US-09-514-247A-10
; Sequence 10, Application US/09514247A
; Patent No. 6365361
; GENERAL INFORMATION:
; APPLICANT: TANABE SEIYAKU CO. LTD.
; APPLICANT: TANIGUCHI, Tomoyasu
; APPLICANT: MIZUKAMI, Junko
; TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPAR
; FILE REFERENCE: TANIGUCHI=6
; CURRENT APPLICATION NUMBER: US/09/514,247A
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT/JP98/03734
; PRIOR FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: JP231084/1997
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
; LENGTH: 2442
; TYPE: PRT
; ORGANISM: human
; US-09-514-247A-10

```

Query Match 6.8%; Score 210.5; DB 4; Length 2442;

Best Local Similarity 21.2%; Pred. No. 4.7e-09; Indels 239; Gaps 32;

Matches 143; Conservative 80; Mismatches 213; Indels 239; Gaps 32;

```

Qy 36 ELSTGSSGHDSSLFEDKND--HDKHDKRRKKKKKKGEKQIPGEKGRKRRVKED--- 88
Db 982 ETNSQCGPVPVLEMTETQAEDETPD-----PGESKGEPSSEMMEDLDLG 1028
Qy 89 --KKKRRDRVNEAEKDLQCHAPVLDLPPEKRLTSLAKQEVET----- 134
Db 1029 ASQVKEETDIAEOKSE-----PMEVD--EKREVVVEKVEEBSGSSNGTASQSTPSQ 1079
Qy 135 -----PLQBALNQLMRQORQPSAF-FSPPTVDFI--AGYSMITIKHPMDFTMK 182
Db 1080 PRKTIKPEEBLROQLMTLEALTRQDPESLPFROPVPOLGLPDYDIKPNPMDSTIK 1139
Qy 183 EKIKNNDDYOSIEELKDNFKLMCTNMTYKPEITTYKAAKLLHSGMKLLSGERTSLQ 242
Db 1140 RKLDTGQYQEPWQVVDVWLMFNNAMLYNRKTSRVYVFCSL-----AEVFEQ- 1194

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QY 243 SIDFMA-----DLQTRKQKQDGTDTSSGSDGCG-----MQREREDSGDA 282
D 1195 SLGVCCKRKRFSPQTLCCYQKQCTIPRDAAYYSYQNRHFFCKCFTEIOGENVTLGD- 1253
QY 283 EAHAFKSPSKENKKKDKMDLDEKFKSNLLE-----REGQOL----- 318
D 1254 -----DPSQPTTISKQFEEK--KNDTLDEPFVDCCKGKMHQICVLHYDIIMPSGF 1306
QY 319 --DRIVESG-----GKTLRLVNSQCFEERKRDGTTTLGLHPVPIV 361
D 1307 VCDNCKLKTGRPKRKNFSARLQTRRLGNHLEDRVNFRLRQN-----HP----- 1352
QY 362 GEPYCLVRLGTMTRQLSGVNTLQGFEDKRNKYTPVL---YLYNGPYSSYAPH-YDST 417
D 1353 -EAEVVRVYVASS-----DKTVEVKRQMSKRFVDSGEMSESPYRTKAL 1396
QY 418 FANISKDSDLIY-----STYGEDSLPDS-----FSIHEFLATC---QDYPYVAD 461
D 1397 FAFBEIDGVDCYCFGMHVQEVGSDCPNTRRYVYSYLDLSIHFRPRCLRTAVYHEILIG 1456
QY 462 SLIDLVLTKG---GHSRTLQEMEMSLPEDEG---HRTLDTGKMEQITEVEPPGRLD- 512
D 1457 YLEVYKKLGYVTGHI-----MACPSEGGDYIFHCHPPD-----QKIPKPKLOE 1501
QY 513 -----SSTODRLTALAKAVTNFGVVEVDFSEBEAEIFQKXLD 549
D 1502 WYKQMLDKAFARIRIHDKDIFKQATEDRLTSAKELPYF-----EGDFPVPVLEE 1551
QY 550 TTRLRLRELQEAONER 564
D 1552 S---IKELQEEER 1563

```

```

RESULT 4
US-08-194-468-2
; Sequence 2, Application US/081944468
; Patent No. 5750336
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
; TITLE OF INVENTION: RESPONSIVE GENES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Precity, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,468
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)-546-4737
; TELEFAX: (619)-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-194-468-2
Query Match 6.4%; Score 198; DB 1; Length 2441;
Best Local Similarity 19.9%; Pred. No. 5.9e-08;
Matches 139; Conservative 93; Mismatches 219; Indels 248; Gaps 29;

QY 32 NEYTELSTGSSGSDSLFEDKNDHKDKRRKKRKKGKEKOIPGEEKRRRRYKED--- 88
D 971 NRPVPTSTVSAFTSS--QQPGPDVPLMEKTEVQTDADAPPEFTESGGEERSEMEEDLQ 1028
QY 89 ---KKRRDRVNEAEKDIQCHAPVRLDLPPEKPLTSLAKQEEVQF----- 134
D 1029 GSSQVKEETDTTQKSEP-----MEVBEKKPEVKEVAKSEBENSNDTASQSTSPS 1079
QY 135 -----PLQALNQLMRQLQKDPKSAF--PSFPTDRI--APGSMIHKPMDSSTM 181
D 1080 QPRKKIFKPEELRQALPTEALYRDPESLPFRQVPDQLGIPDYFDIVKXNMDLSTI 1139
QY 182 KEKIKNNDYOSIELKDNFLMCTNAMIYNNKPEYIYKAKKLLHSGMKILSGERISLK 241
D 1140 KRKLDTGQYQEPQYQYVDVLMFNNAVLNKRKTSRYVKFCSKL---ASVFEQE-IDPYM 1194
QY 242 QSIDPMADLQKTRKQKQDTP-----SQSGEDGCGW---QERE 277
D 1195 QSLGYCCG---RKYERSPQTLCCYQKQCTIPRDAAYYSYQNRHFFCGKCFTEIOGENV 1250
QY 278 DSGDAEHAHAFKSPSKENKKKDKMDLDEKFKSNLLE-----REGQOL----- 318
D 1251 TLGD-----DPSQPTTISKQFEEK--KNDTLDEPFVDCCKGKMHQICVLHYDI 1302
QY 319 -----DRIVESG-----GKTLRLVNSQCFEERKRDGTTTLGLHP 356
D 1303 WPSGFVCDNCKLKTGRPKRKNFSARLQTRRLGNHLEDRVNFRLRQN-----HP 1353
QY 357 VDPVGEPCYCLVRLGTMTRQLSGVNTLQGFEDKRNKYTPVL---YLYNGPYSSYAPH 413
D 1354 -----EAGEVFRVYVASS-----DKTVEVKRQMSKRFVDSGEMSESPY 1392
QY 414 -----YDSFANISKDSDLI-----YSTYGEDSLPDSFSIHEFLAT 451
D 1393 RTALFAFBEIDGVDCYCFGMHVQDGLALPHQIQGVYISYLD-----SIHFRPR 1444
QY 452 C-----QDYPYVADSLIDLVLTKG-----HSRTLQEME 480
D 1445 CLRTAVYHEILIGYLEVYKKLVYTAHIAACPSBGGDYIFHCHPPQKIPKPKLOEY 1504
QY 481 MSLPDEGHTRLDTGKMEQITEVEPPGRLDSTODRLTALAKAVTNFGVVEVDFSEEA 540
D 1505 KQMLDKAFARIRINDYKDI-----FKQANEDRLTSAKELPYF-----EG 1543
QY 541 EIFQKLDLDTLRLRELQEAONER-----LSTRPPGN 572
D 1544 DFWPVPVLEES---IKELQEEERKKEESTASSETPEGS 1579

RESULT 5
US-08-961-739-2
; Sequence 2, Application US/08961739A
; Patent No. 6063583
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/08/961,739A
; CURRENT FILING DATE: 1997-10-31
; EARLIER APPLICATION NUMBER: US 194,468
; EARLIER FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatcSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2441
; TYPE: PRT
; ORGANISM: Mus

```

FEATURE:
NAME/KEY: VARIANT
LOCATION: (1) (2441)
OTHER INFORMATION: Xaa = Any Amino Acid
US-08-961-739-2

Query Match 6.4%; Score 198; DB 3; Length 2441;
Best Local Similarity 19.9%; Pred. No. 5.9e-08;
Matches 139; Conservative 93; Mismatches 219; Indels 248; Gaps 29;

QY 32 NEVELSTGSGHSSLFEDKNDHDKKRRKKRKKGEKQIPGEKRRRRKED--- 88
DB 971 NRVPSTVTSATSS--QOPGPDVPMLEKTEVQTDABEPPTSGEPRSEMMEDLQ 1028
QY 89 ---KKRRDRVENEAEKDLQCHAPVRDLDPPEKPLTSSLAKEVEQT----- 134
DB 1029 GSSQVKEETDTTEQKSE-----MEVEKKEPVKEAKEEENSNDTASQSTSPS 1079
QY 135 -----PLOEALNQLMRQLQKDPSPAF-FSPVYDFI--APGYSMITIKHPMDFSTM 181
DB 1080 QPRKKIFKPEELRLQALMPTLEALYQDPESLPFRQVPDPLGIDYFDIVKPMDLSTI 1139
QY 182 KEKIKNDYOSIEELKDNFKLCTNMTYKPEITYYKAAKLLHSGMKILSQRISLQ 241
DB 1140 KRKLDTQGYQEPWQYVDVRLMFNNAMLYNRKTSRYKFCSKL---AEVFEQ-IPVM 1194
QY 242 QSIDPMADLQTRKQKGTDT-----SQSGEDGCGM---QRRRE 277
DB 1195 QSLGCGG---RKYEFSPTLCCYQKQCTIPDAAYYSQNRVHFCGKCFTEIQGENV 1250
QY 278 DSGDAEAAFPSPSKENKKDKMLDEKFSNNLE-----REOQL----- 318
DB 1251 TLGD-----DPSQPTTISKQFEKK-KNDTLDPEPFVDCKEGCKGMQICVLHYDI 1302
QY 319 ---DRIVKESG-----GKLTRELVNSQCEFERRRKPDGTTTGLLHP 356
DB 1303 WPSGFVDCNCLKTKGRPRKENKFSAKRLQTRRLGNHLEDVNNFLRRQN-----HP 1353
QY 357 VDPVIGEPGYCLVRLGWTGRLQSGVNTLQGFKEKRNKKTVPV---YLVNGPYSSVAPH 413
DB 1354 ---EAGEVFRVAVAS-----DKTVEKVRPKMSRFRVDSGEMSESPFY 1392
QY 414 -----YDSTFANISKDSDLI-----YSTYGEDSDLPSPFSIHEFLAT 451
DB 1393 RTKALFAFEELIDGVDFCFGMHVQDTALIAHQIQGCVYISYLD-----SIHFRPR 1444
QY 452 C-----QDYRYMADSLDLVLTKG-----HSRTLQEME 480
DB 1445 CLRTAVYHEILIGLYEVKKLVYVTAHMACPSEGDYIFHCHPPDQIKPKPRRLQEWY 1504
QY 481 MSLEDEBCHTTLDTGKEMEQITEVEPRGRDSSQDRLALKAVTNGVVEVFDSSEA 540
DB 1505 KKMIDLKAFARIINDYKDI-----FKQANEDRLTSAKELPYF-----EG 1543
QY 541 EIFOKLDETRRLRELQEAQNER-----LSTRPPGN 572
DB 1544 DFMPNVLEES---IKELQEEERKKEESTAASETPEGS 1579

RESULT 6
US-09-514-247A-8
Sequence 8, Application US/09514247A
Patent No. 6365361
GENERAL INFORMATION:
APPLICANT: TANABE SEIYAKU CO. LTD.
APPLICANT: TANIGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, Junko
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPR
FILE REFERENCE: TANIGUCHI-6
CURRENT APPLICATION NUMBER: US/09/514, 247A
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24

PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 2441
TYPE: PRT
ORGANISM: mouse
US-09-514-247A-8

Query Match 6.4%; Score 198; DB 4; Length 2441;
Best Local Similarity 19.9%; Pred. No. 5.9e-08;
Matches 139; Conservative 93; Mismatches 219; Indels 248; Gaps 29;

QY 32 NEVELSTGSGHSSLFEDKNDHDKKRRKKRKKGEKQIPGEKRRRRKED--- 88
DB 971 NRVPSTVTSATSS--QOPGPDVPMLEKTEVQTDABEPPTSGEPRSEMMEDLQ 1028
QY 89 ---KKRRDRVENEAEKDLQCHAPVRDLDPPEKPLTSSLAKEVEQT----- 134
DB 1029 GSSQVKEETDTTEQKSE-----MEVEKKEPVKEAKEEENSNDTASQSTSPS 1079
QY 135 -----PLOEALNQLMRQLQKDPSPAF-FSPVYDFI--APGYSMITIKHPMDFSTM 181
DB 1080 QPRKKIFKPEELRLQALMPTLEALYQDPESLPFRQVPDPLGIDYFDIVKPMDLSTI 1139
QY 182 KEKIKNDYOSIEELKDNFKLCTNMTYKPEITYYKAAKLLHSGMKILSQRISLQ 241
DB 1140 KRKLDTQGYQEPWQYVDVRLMFNNAMLYNRKTSRYKFCSKL---AEVFEQ-IPVM 1194
QY 242 QSIDPMADLQTRKQKGTDT-----SQSGEDGCGM---QRRRE 277
DB 1195 QSLGCGG---RKYEFSPTLCCYQKQCTIPDAAYYSQNRVHFCGKCFTEIQGENV 1250
QY 278 DSGDAEAAFPSPSKENKKDKMLDEKFSNNLE-----REOQL----- 318
DB 1251 TLGD-----DPSQPTTISKQFEKK-KNDTLDPEPFVDCKEGCKGMQICVLHYDI 1302
QY 319 ---DRIVKESG-----GKLTRELVNSQCEFERRRKPDGTTTGLLHP 356
DB 1303 WPSGFVDCNCLKTKGRPRKENKFSAKRLQTRRLGNHLEDVNNFLRRQN-----HP 1353
QY 357 VDPVIGEPGYCLVRLGWTGRLQSGVNTLQGFKEKRNKKTVPV---YLVNGPYSSVAPH 413
DB 1354 ---EAGEVFRVAVAS-----DKTVEKVRPKMSRFRVDSGEMSESPFY 1392
QY 414 -----YDSTFANISKDSDLI-----YSTYGEDSDLPSPFSIHEFLAT 451
DB 1393 RTKALFAFEELIDGVDFCFGMHVQDTALIAHQIQGCVYISYLD-----SIHFRPR 1444
QY 452 C-----QDYRYMADSLDLVLTKG-----HSRTLQEME 480
DB 1445 CLRTAVYHEILIGLYEVKKLVYVTAHMACPSEGDYIFHCHPPDQIKPKPRRLQEWY 1504
QY 481 MSLEDEBCHTTLDTGKEMEQITEVEPRGRDSSQDRLALKAVTNGVVEVFDSSEA 540
DB 1505 KKMIDLKAFARIINDYKDI-----FKQANEDRLTSAKELPYF-----EG 1543
QY 541 EIFOKLDETRRLRELQEAQNER-----LSTRPPGN 572
DB 1544 DFMPNVLEES---IKELQEEERKKEESTAASETPEGS 1579

RESULT 7
US-09-535-008-75
Sequence 75, Application US/09535008
Patent No. 6465629
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavligian, Sean V.
APPLICANT: Teng, David H.-F.
TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
TITLE OF INVENTION: AND OTHER CANCER TYPES

Db 1665 EQEE-DR 1670

RESULT 10

US-08-227-536-2
Sequence 2, Application US/08227536

Patient No. 5658784

GENERAL INFORMATION:

APPLICANT: Ecken, Richard

APPLICANT: Ewen, Mark

TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION

TITLE OF INVENTION: FACTOR P300 AND USES OF P300

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes

STREET: Ten Post Office Square

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/227,536

FILING DATE: 14-APR-1994

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Williams Ph.D., Kathleen A.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: DFCI-308XX

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-2290

TELEFAX: (617) 451-0313

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2414 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-227-536-2

Query Match 6.2%; Score 190.5; DB 1; Length 2414;

Best Local Similarity 20.4%; Pred. No. 2,7e-07;

Matches 130; Conservative 83; Mismatches 249; Indels 175; Gaps 26;

38 STGSGHDSLFEDKNDHDKRRKKRKGKQIPGEEGRRRRYKEDKKRRDRV 97

956 STSTEVNSQALAEK---QPSQEVKMEAKMEVDQPEPADTQPEDISSEKVEDCKMESTET 1012

98 ENELKQLQCAVPRDLPREKPLTSLA---KOEVEQVPLQELANQLKROLQKQPS 153

1013 E-ERSTELKTEIKEEDQPTSATQSSAPQSQKKKIFKPEELKQALMPTLEALYRQDPE 1071

154 AF-PSFPTDFI--APGYSMIIKHPMDFTWKERIKNNDYOSIELKDNFKLMCTNMIY 210

1072 SLPRQVVDPLDGLIPQFDIVKSPMDSTIKRKLDTGQVPEPMQYVDIWMNNMMLY 1111

211 NKPEITVYKAAKKLLHSGMKILSQERISLQSLKQSIDFMA-----DLQKTRKO 256

1132 NKRTRSVYKYSKSL---SEVFEQE-IDPVNQSLGCGRKLESPQTLCCYQKQLCTIP 1186

257 KDGCDTQSQSGDGC-----WQREBRESGDAEAHAFSPKEN-KKKDKMLDKF--K 307

1187 RDAIVYISQNRHYHCEKCFNEIQGESVSLGDPSPQPTTKNEQFSKRRKNDTLDELFE 1246

308 SNNLEBEOEL-----DRIVKESG-----GKLTRELIV 334

1247 CTGCRKMHQICVHLHETIWPAGFVDCGLKKSARTRKKNKFSKRLPSTRLGLTFLENRV 1306

QY 335 NSOCFERRRKPDGTTTLGLHPVDPIYGERGYCLVRLGMTTGRLOSQVNTLQGFKEKRN 394

Db 1307 NDFLRQNHPESEGEVTVRVVHSDKYVE-----VKRGMARVDSG-EVASEF----- 1353

QY 395 KATPVLYLNGPYSSAAPHYSSTFANISKSDSLIY-----STYGBDSDLPSD----- 442

Db 1354 -----PRTYA-----LFAFEIDGVDLCFRGMHVGESDCCPPNQRVYISY 1397

QY 443 -FSIHEFLATC---QDYPYMADSLIDVLITKGHSRLQEMMSLPEDEGHTRLDTGKE 498

Db 1398 LDSVHFRRPKLRTAVYHEILLI-GYLEYVKQLGYT-----TSHIACPPSEG 1443

QY 499 MEQITEVEPPGR-----LD-----SSTODRLALKAVTN 527

Db 1444 DDTIFHCHPDDQKIPKPKLQEWYKKMLDKAVSERIYHDKDIFKQATERTLSAKELPY 1503

QY 528 FGVPVEVFESEBAEIPQKLDDETRRLRLQEAQNER 564

Db 1504 F-----EGDFWENVLEES---IKELQGEER 1527

RESULT 11

PCT-US95-04682-2

Sequence 2, Application PC/TUS9504682

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: NUCLEIC ACID ENCODING TRANSCRIPTION

TITLE OF INVENTION: FACTOR P300 AND USES OF P300

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes

STREET: Ten Post Office Square

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04682

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,536

FILING DATE: 14-April-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Holliday C. Heine, Ph.D.

REGISTRATION NUMBER: 34,346

REFERENCE/DOCKET NUMBER: DFCI-308X999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-2290

TELEFAX: (617) 451-0313

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2414 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-04682-2

Query Match 6.2%; Score 190.5; DB 5; Length 2414;

Best Local Similarity 20.4%; Pred. No. 2,7e-07;

Matches 130; Conservative 83; Mismatches 249; Indels 175; Gaps 26;

38 STGSGHDSLFEDKNDHDKRRKKRKGKQIPGEEGRRRRYKEDKKRRDRV 97

956 STSTEVNSQALAEK---QPSQEVKMEAKMEVDQPEPADTQPEDISSEKVEDCKMESTET 1012

QY 98 ENEAKDLOCHAPVRLDLPEKPLTSSLA---KQEEVEQTPLOEALNOLMRQOROPS 153
Db 1013 E-ERSTELTEIKEEEDQPSATQSSPAPQSSKKKIFKPEBELRQALMPLTBLVRQDPE 1071
QY 154 AF-FSPVYPTFI--ABGSMILKHPMDFSTMEKEKIKNDYQSIIEBKONFLMCTNAMY 210
Db 1072 SLFPRQVDPDQLGIPDYFPIVKS PMDLSTIKRLDGTQYQEPQYVDDIWMENNAWLY 1131
QY 211 NKEPETIYKAKKLLHSGMKILSGERIQSLKQSIDEMA-----DLQTRKQ 256
Db 1132 NRTSRVYKTCCKL---SEVFEQD-IDPMQSLGICCGKRLKLEPOTLCCYQKOLCTIP 1186
QY 257 KQDGTDSQSGEDGCG---WQEREDSGDAEAAFKSPSKEN-KKKDXMLEDKF--K 307
Db 1187 RDATYYSYQKRYHFCCEKCFNEIOGESVSLDDPSQPTTINKQFGRKNDTIDPELFE 1246
QY 308 SNNLEREQDL-----DRIYEGS-----GKLTIRLY 334
Db 1247 CTECGRMHQICVLHHEIWPAGFVCDGLKKSARTKKNKFSKRLPSTRLGTFLENRY 1306
QY 335 NSQCEFERRRKPDGTTLLGLHPVDPIYGEBOYCLVRLGMTTGRLOSGVNTLQGFKEKRN 394
Db 1307 NDLRQRNHPESGBVTVRVVHASDKTVE-----VKFGMARFVDSG-EKAESEF----- 1353
QY 395 KATPVLYLNGPYSSYAPHYDSTFANISKDSDLIY-----STYGEDSDLPSD----- 442
Db 1354 -----PRTKA-----LEAPEIDGVLCFGMHVQYSGSPRPNGRVYISY 1397
QY 443 -FSIHEFLATC---QDYPVMADSLDLVLTGKHSRTLOEMWSLPEDEGHTRLDTGKE 498
Db 1398 LBSVHFPRKCLRTAVVHEILI-GYLEVYKKGIVT-----TGHIMACPSSEG 1443
QY 499 MEQITEVERPGR-----LD-----SSTORLALAKAVTM 527
Db 1444 DDYTFHCPDQKIPKPKRLQEWYKMLDKAVSERIVHDYKIFKQATEDRLTSAKELPY 1503
QY 528 FGVPVEFVDESEAEIIFOQKLDFTRLRLRELOAQRNER 564
Db 1504 F-----EGDFWPNVLEES---IKELQEEBER 1527

RESULT 12
US-09-535-008-65
; Sequence 65, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-008-65

Query Match 6.2%; Score 189.5; DB 4; Length 1679;
Best Local Similarity 22.3%; Pred. No. 1.9e-07;
Matches 80; Conservative 62; Mismatches 119; Indels 99; Gaps 17;
QY 2 GKXKHKH--KSDKHLVEYVEKPLKVLKYGNEVTELST-----GSS 42
Db 1370 GSHRRKEVDYSDLSLTKQWKL-----KITGKDIDHTASVARGLOFQGLQFCTRAK 1422
QY 43 GHDSLFEEDKND--HDKHKDRKRRKKRKKGKQIPGEEKGRRRRVKKEDKKDRDRVENE 100

Db 1423 AIBEGTLEIEIEEVROKSSRRKRRKSDAGSSTPTTS---TRSRDKDESKQKKGRPP 1479
QY 101 AERDLOCHAPVRLDLPEKRP-LTSSLAQOEVEQTPLOEALNOLMRQORKDSAPFSFP 159
Db 1480 AER-----LSPNPNLTK---KKMKIVDAVIXKXSSGSLQSL---EVFLQLP 1521
QY 160 VTFIAPGYSMILKHPMDFSTMEKEKIKNDYQSIIEBKONFLMCTNAMYKPEITYYK 219
Db 1522 SRKEL-PEYIELRKRVDFKIKERIRNKRYSRLNDLEKDWMLCONAQTFNLGSLIYE 1580
QY 220 AAKKLLHSGMKILSGERIQSLKQSIDFMADLOKTRKQKGTDTDSQSGEDGCGWQEREDS 279
Db 1581 DS-----IYLQSVFTSVRQIE-----KEDD-----SEGES-----EEEEE 1612
QY 280 GDAAEAAFKSPSKENKK--DKDMLEDKF-----SNNLEREQDLR 320
Db 1613 GEEEGESESESRVYKIKLGRKEKADRLKGRRRRPSGRAPVVSDDSEEOEB-DR 1671

RESULT 13
US-09-535-008-67
; Sequence 67, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 1646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-008-67

Query Match 6.1%; Score 188.5; DB 4; Length 1646;
Best Local Similarity 22.3%; Pred. No. 2.2e-07;
Matches 76; Conservative 52; Mismatches 112; Indels 101; Gaps 13;
QY 7 KHKSDKHLVEYVEKPLKVLKYGNEVTELSTGSSGHDSLFEEDKNDHKDRKRRK 66
Db 1372 RHRKEVDYSDLSLTKQWKLAIIEGTLEIEIE-----EYVQKSSRRKRD 1416
QY 67 KXGKQIPGEEKGRRRRVKKEDKKRRDRVENEAKDLOCHAPVRLDLPEKRP----- 120
Db 1417 SDAGSSTPTTS---TRSRDKDESKQKKGRPREAK-----LSPNPNLTCKM 1462
QY 121 --LTSSLAQOEVEQTPLOEALNOLMRQORKDSAPFSFPVYTFIAPGSMILKHPMD 178
Db 1463 KKIIVAVIRYKQSSGRLSEVFLQPL--SRKE-----LPEYIELIRKRVDF 1506
QY 179 STMEKEKIKNDYQSIIEBKONFLMCTNAMYKPEITYYKAKKLLHSGMKILSGERIQ 238
Db 1507 KIKERIRNKRYSRLNDLEKDWMLCONAQTFNLGSLIYEDS-----IYLQSVFT 1557
QY 239 SLKQSIDFMADLOKTRKQKGTDTDSQSGEDGCGWQEREDSGDAEAAFKSPSKENKK- 297
Db 1558 SVRQIE-----KEDD-----SEGES-----EYVQKSSRRKRD 1598
QY 298 -DKDMLEDKF-----SNNLEREQDLR 320
Db 1599 GRKEKADRLKGRRRRPSGRAPVVSDDSEEOEB-DR 1638

RESULT 14

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US-09-535-008-77
; Sequence 77, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; TITLE OF INVENTION: AND OTHER CANCER TYPES
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 77
; LENGTH: 1681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-008-77

Query Match      6.1%; Score 188.5; DB 4; Length 1681;
Best Local Similarity 21.8%; Pred. No. 2.3e-07;
Matches 81; Conservative 59; Mismatches 111; Indels 121; Gaps 16;

QY 2 GKXKHKH--KSDKLYEYVEKPLKLVKYGNEVTELSGSSGHDSLFE----- 50
DB 1370 GSRHKEVDYSDSLTEKQWLK-----KITGKDINH--TASSVARGIQFQRLQFCTRA 1420
QY 51 -----DKNDHDKHDKRKRKKKGEKQIPGEEKRKRKYVEDKKRDRD 95
DB 1421 SKTLKAIIEGTEIEEVEVOKKSRKRKRDSDGSSSTPTTS---TSSRDKDDSKKQK 1477
QY 96 RVENAEKDLQCHAPVRLDLPPEKP-----LTSSLAQEVEVQTPLOALNQLMRQL 147
DB 1478 RGRPPAK-----LSPNPNTLKQKKIVDAVIKYKDSGQSLSEVFQLP--- 1523
QY 148 QKDPSPAFSPFPTDFIAPGYSMIYKHPMDSTMEKIKANDYQSIIEELKDNFGLMCTNA 207
DB 1524 SRKE-----LPEYELIRKPVDFPKIKERIRNHKYSRLNDLEKDVMLLCQNA 1570
QY 208 MIVNKPETIYKAKKLLHSGMKILISOERISLQSIDFMADLQTRKQKQDGTDSQSSE 267
DB 1571 QTFNLEBSLIYEDS-----IVLOSFTSVRQKIE-----KEDD-----SEGE 1607
QY 268 DGGCQOREEDSGDAEHAFAFKSPSKENKK--DKDMLDKPK-----S 308
DB 1608 ES-----EEEEEGEESSESRSVVKYIKLGRKEKAQDRLKGGRRRPSRGRAPVVD 1662
QY 309 NMLREBOQLDR 320
DB 1663 DDSEBOQE-DR 1673

RESULT 15
US-09-535-008-2
; Sequence 2, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; TITLE OF INVENTION: AND OTHER CANCER TYPES
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
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; LENGTH: 1647
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-008-2

Query Match      6.1%; Score 187; DB 4; Length 1647;
Best Local Similarity 23.1%; Pred. No. 3e-07;
Matches 77; Conservative 53; Mismatches 118; Indels 86; Gaps 14;

QY 7 KHSDDHLYEYVEKPLKLVKYGNEVTELSGSSGHDSLPEDKNDHDKHDKRKKR 66
DB 1372 RHRKEVDYSDSLTEKQWLKAIIEGTEIEE-----BEVQKSSRKRRKD 1416
QY 67 KKEGKQIPGEEKRKRKYVEDKKKDRDRVENEAEKDLQCHAPVRLDLPPEKP-LTSSL 125
DB 1417 SDGSSSTPTTS---TSSRDKDDSKKQKGRPPAK-----LSPNPNTLK-- 1460
QY 126 AKQEEVEQTPLOALNQLMRQLOKDPSPAFSPFPTDFIAPGYSMIYKHPMDSTMEKI 185
DB 1461 -KMKIIVDAVIKYKDSGQSLSEVFQLPSSREL-PEYVELIRKPVDFPKIKERI 1514
QY 186 KANDYQSIIEELKDNFGLMCTNAMIVNKPETIYKAKKLLHSGMKILISOERISLQSID 245
DB 1515 RNHKYSRLNDLEKDVMLLCQNAQTFNLEBSLIYEDS-----IVLOSFTSVRQKIE 1565
QY 246 FMADLQTRKQKQDGTDSQSGEDGCGQOREEDSGDAEHAFAFKSPSKENKK--DKDML 303
DB 1566 -----KEDD-----SEGEES-----EEEEEGEESSESRSVVKYIKLGRKEKAQ 1606
QY 304 DKFK-----SNMLREBOQLDR 320
DB 1607 DRLKGGRRRPSRGRAPVVDSEBOQE-DR 1639

Search completed: November 27, 2003, 01:08:59
Job time : 26 secs
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